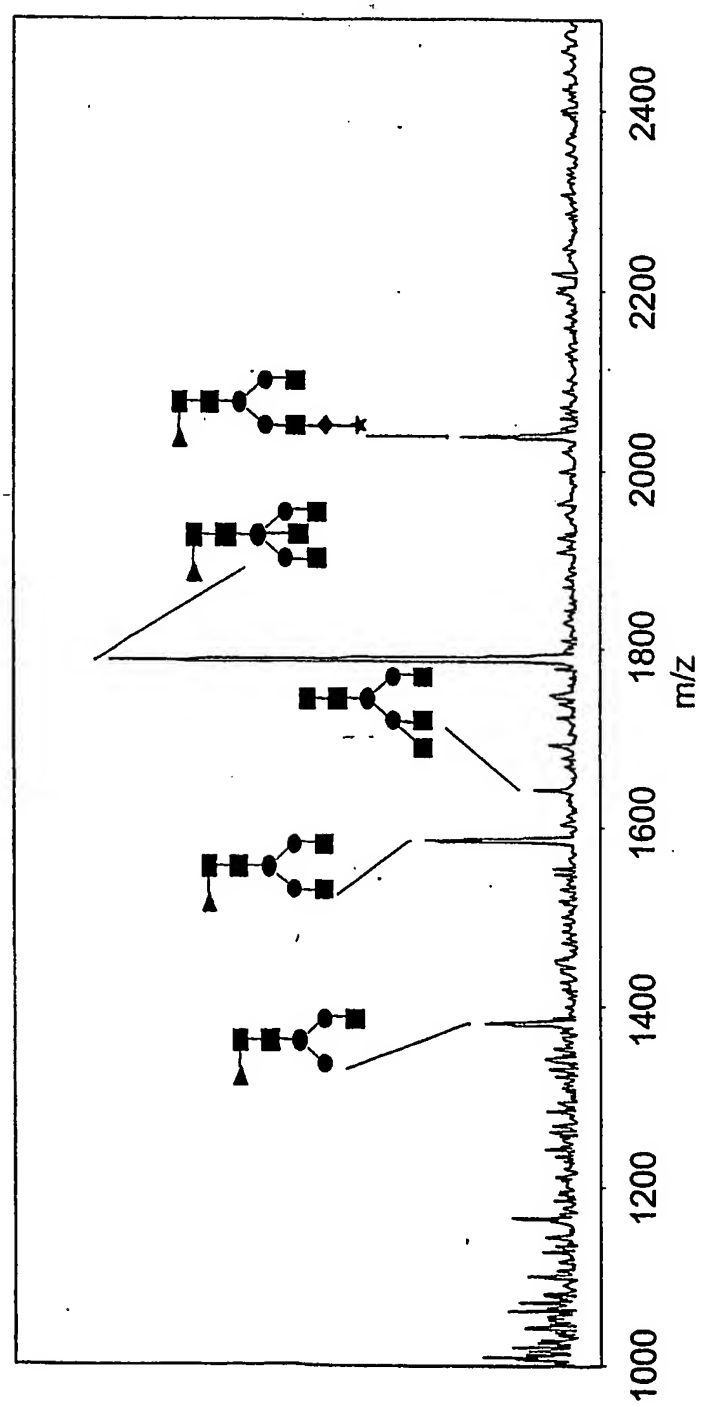

FIG. 111C

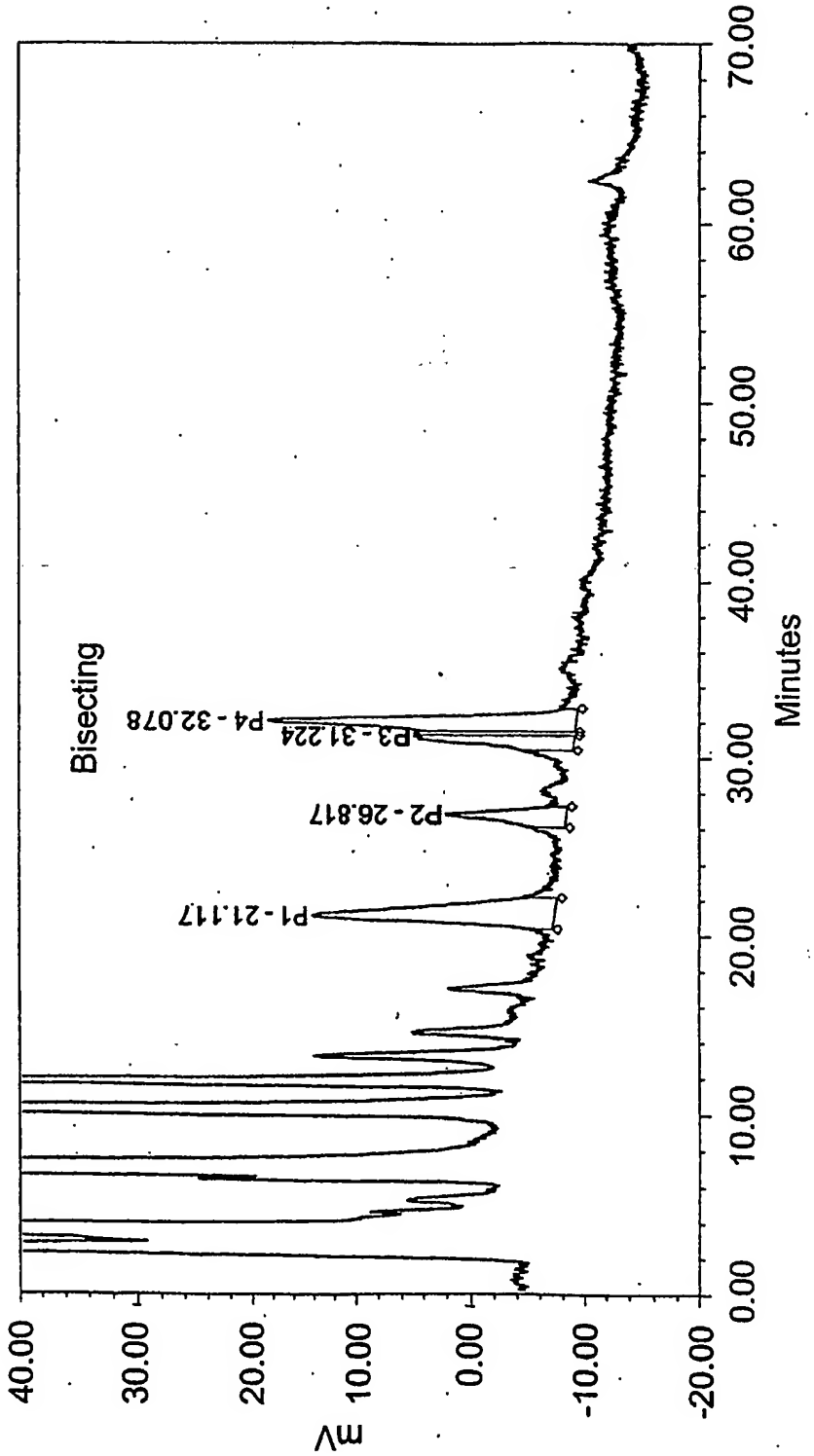
Bisecting
P1-21.117
P2-26.817
P3-31.224
P4-32.078
mV
40.00
30.00
20.00
10.00
0.00
-10.00
-20.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
Minutes

FIG. 112A

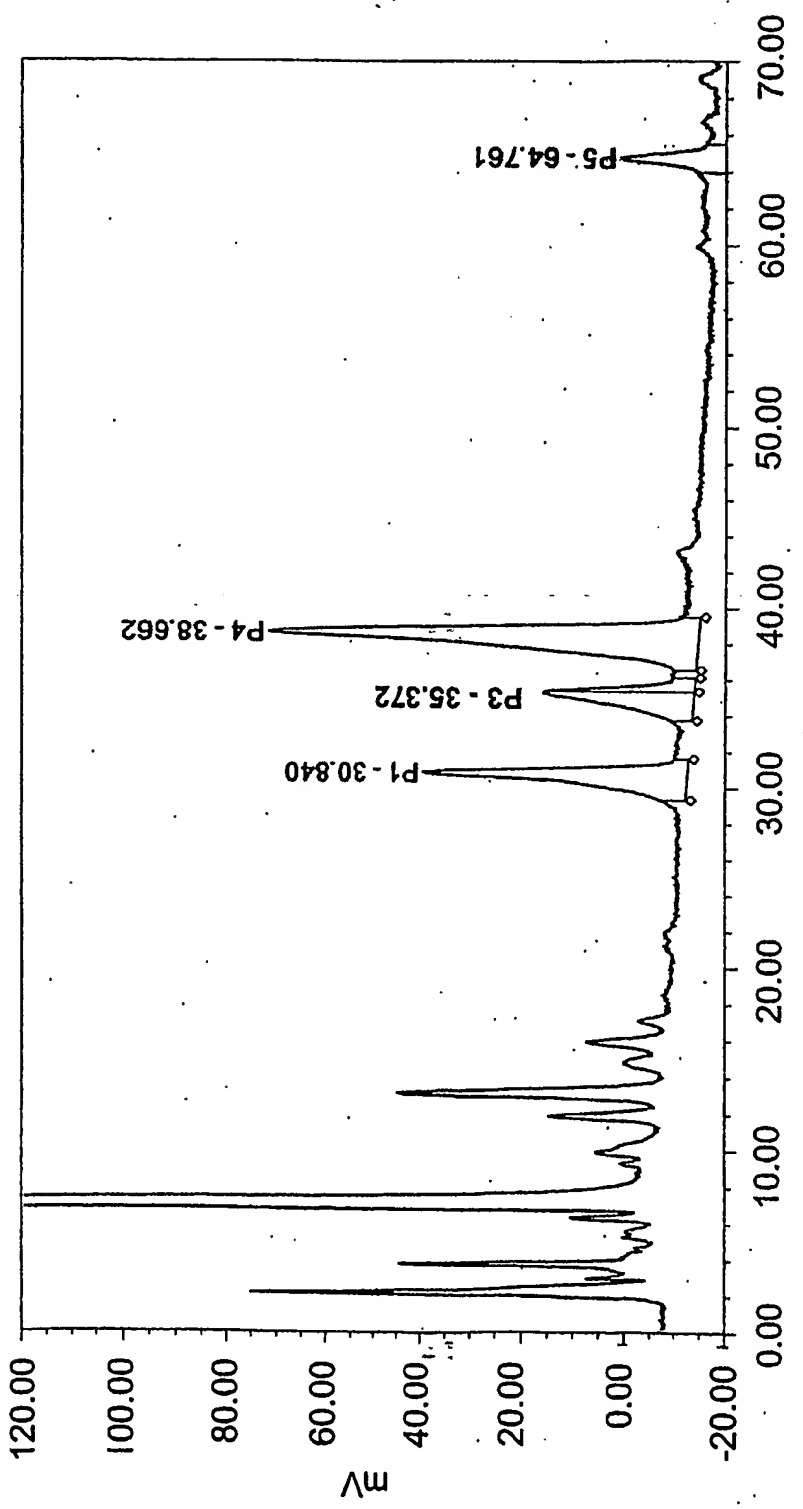
mV
120.00
100.00
80.00
60.00
40.00
20.00
0.00
-20.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
Minutes
P1 - 30.840
P3 - 35.372
P4 - 38.662
P5 - 64.761

FIG. 112B

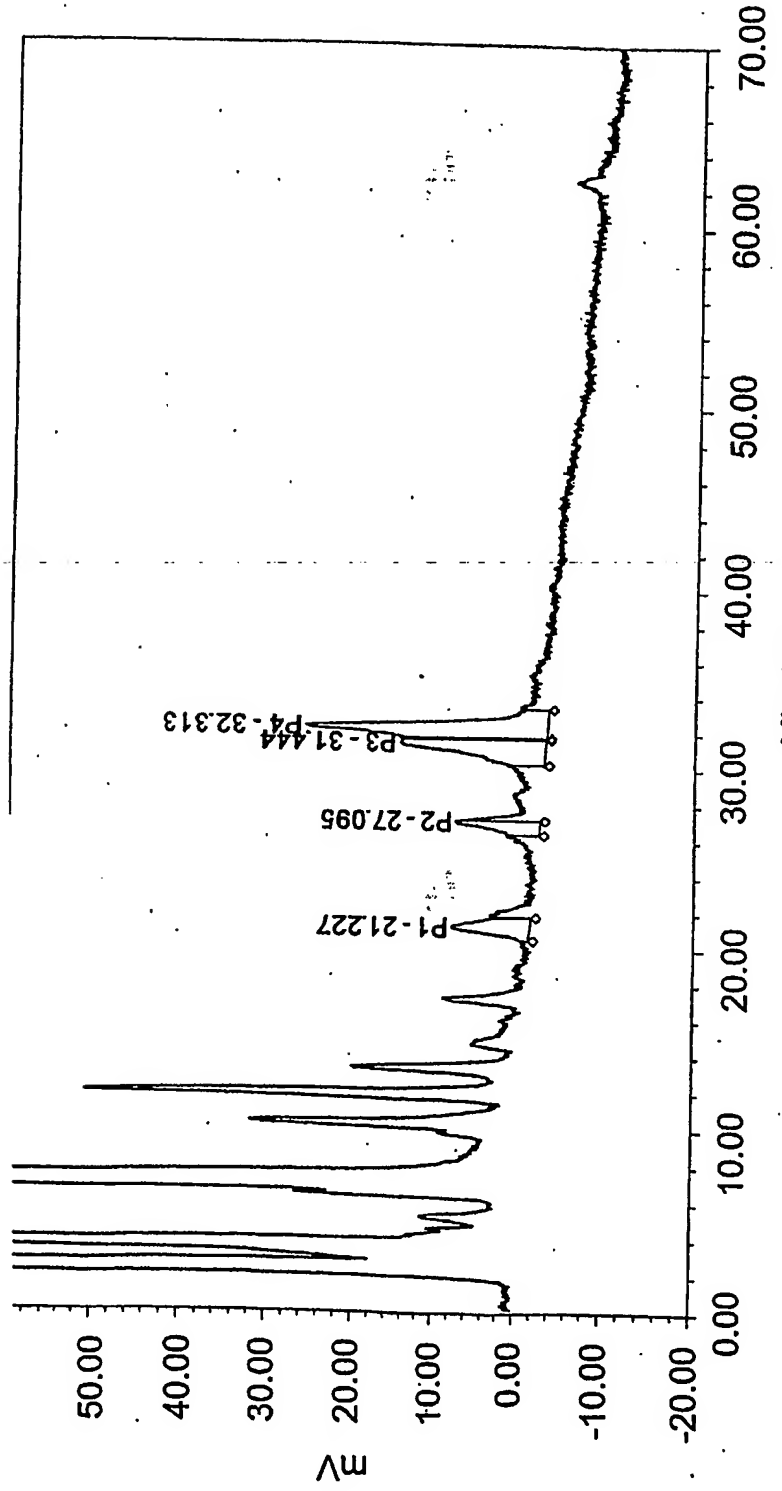
mV
50.00
40.00
30.00
20.00
10.00
0.00
-10.00
-20.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
Minutes
P1-21.227
P2-27.095
P3-31.444
P4-32.313

FIG. 112C

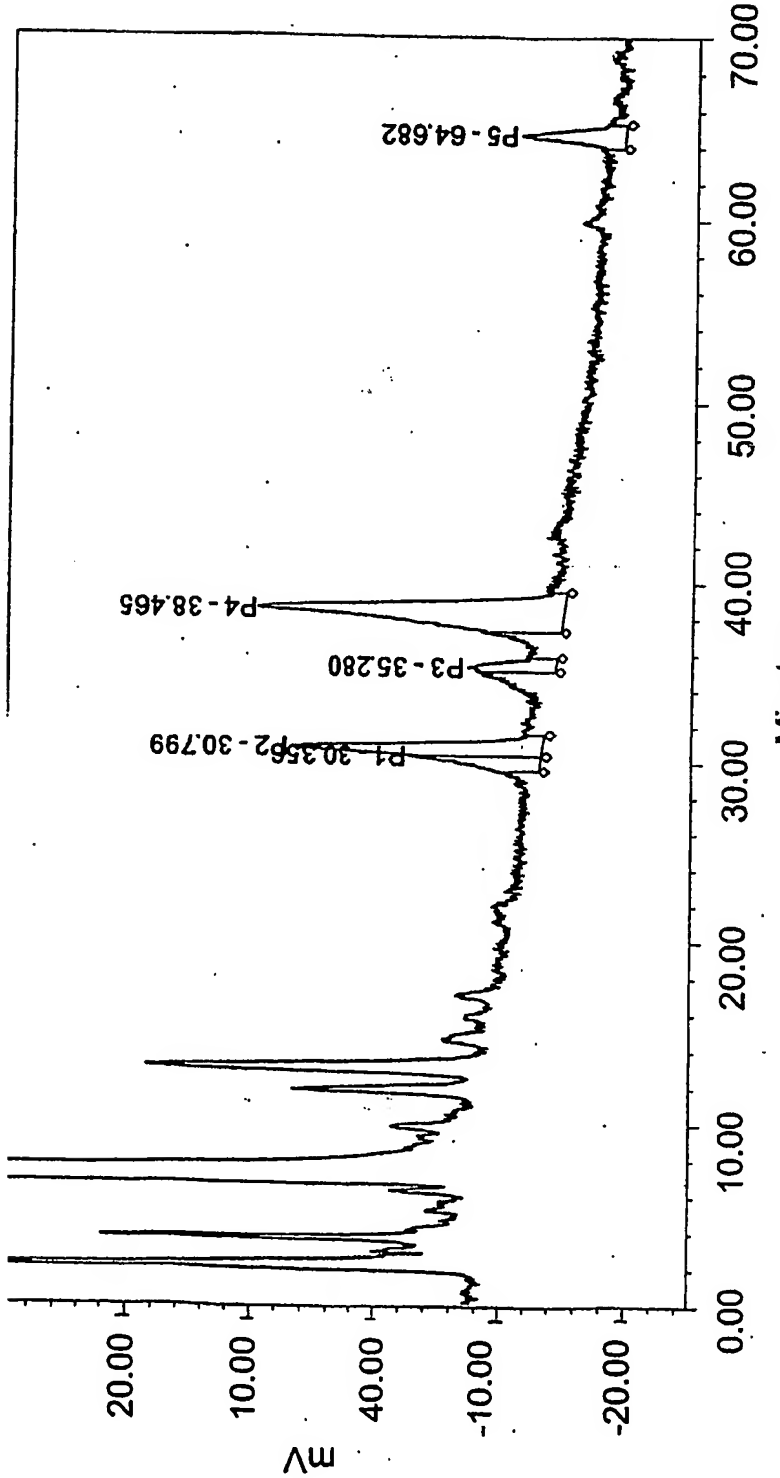
mV
20.00
10.00
40.00
-10.00
-20.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
Minutes
P1 - 30.356
P2 - 30.799
P3 - 35.280
P4 - 38.465
P5 - 64.682

FIG. 112D

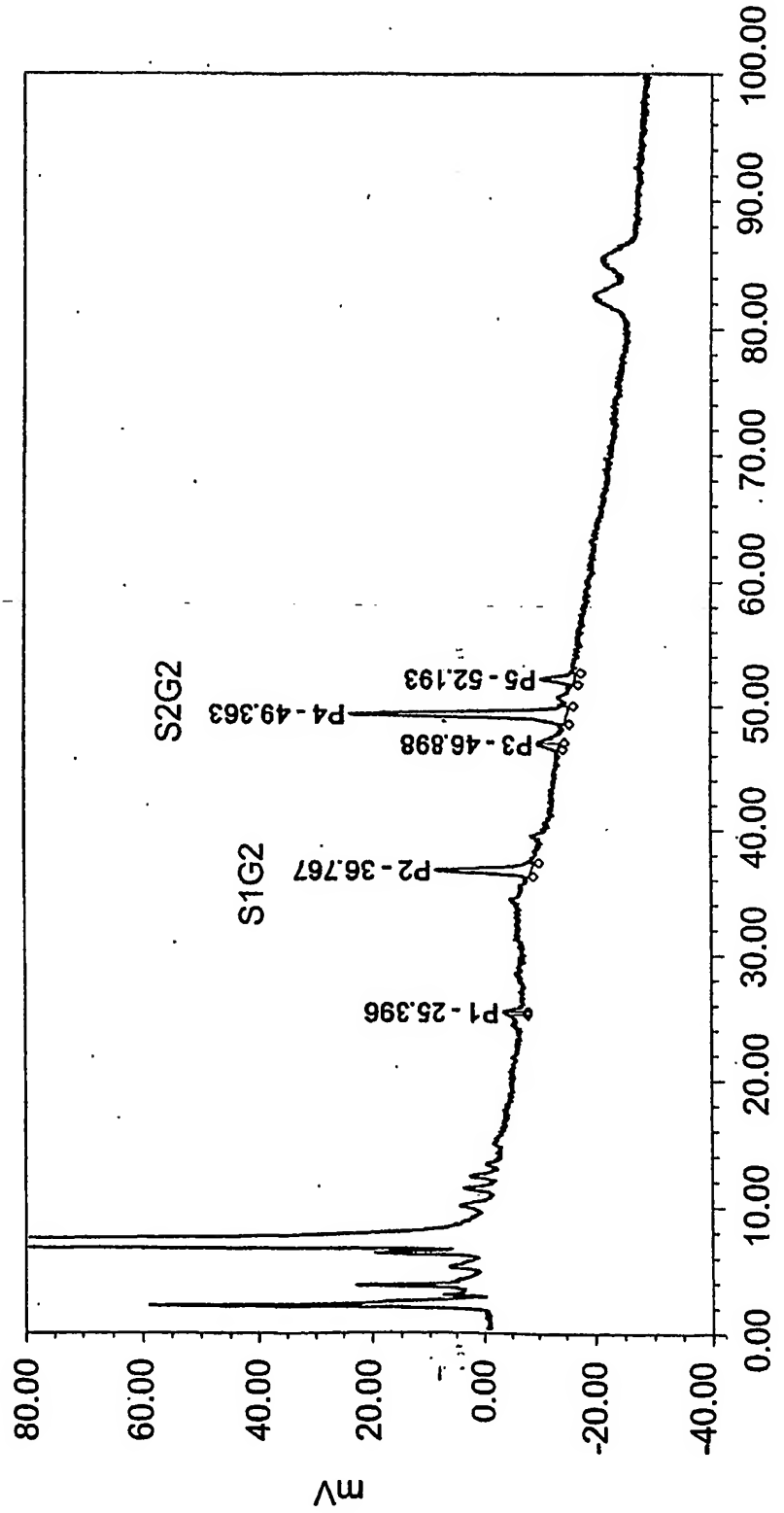
mV
80.00
60.00
40.00
20.00
0.00
-20.00
-40.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
100.00
Minutes
P1 - 25.396
P2 - 36.767
P3 - 46.898
P4 - 49.363
P5 - 52.193
S1G2
S2G2

FIG. 113A

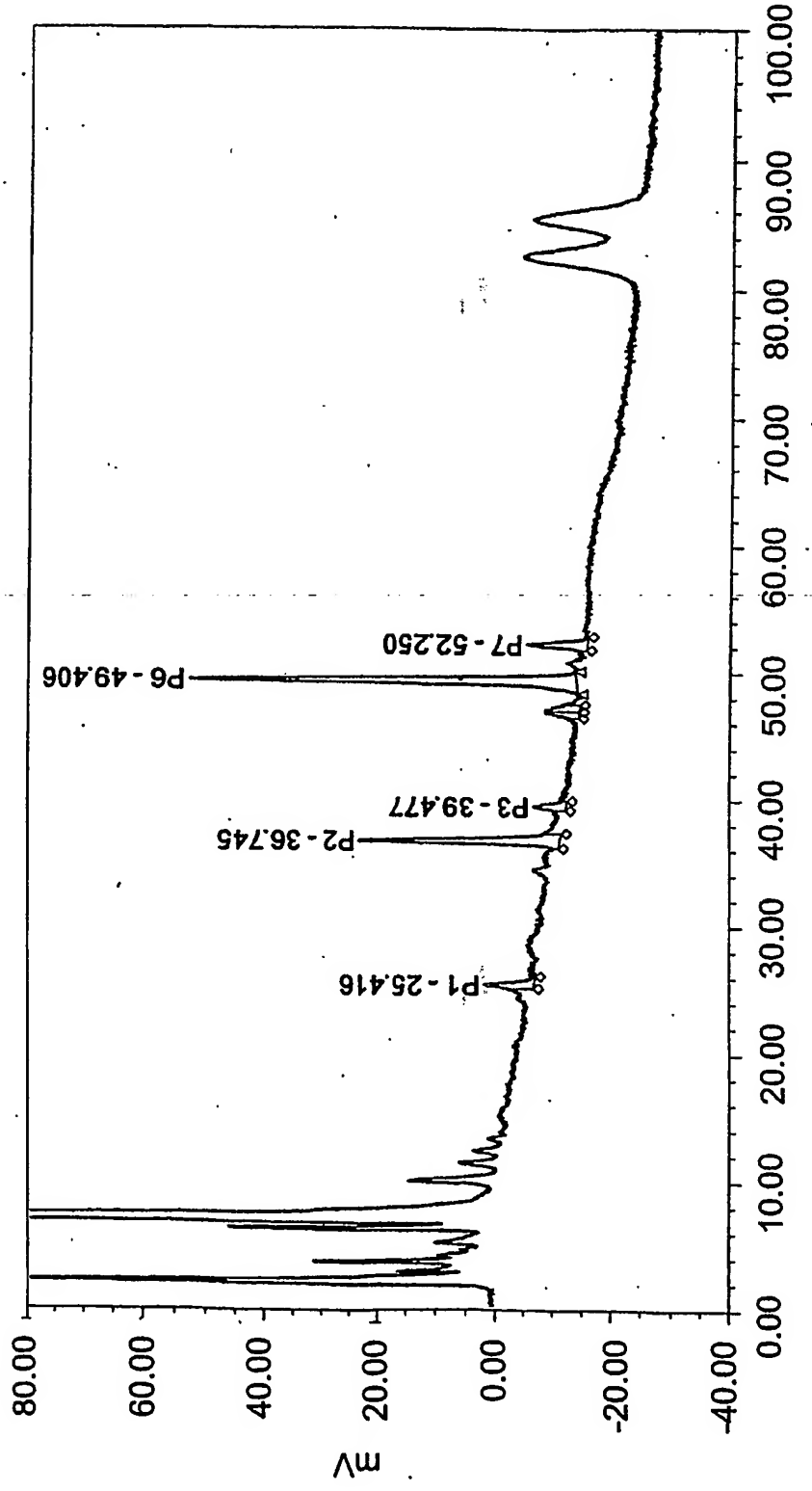
mV
80.00
60.00
40.00
20.00
0.00
-20.00
-40.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
100.00
Minutes
P1 - 25.416
P2 - 36.745
P3 - 39.477
P6 - 49.406
P7 - 52.250

FIG. 113B

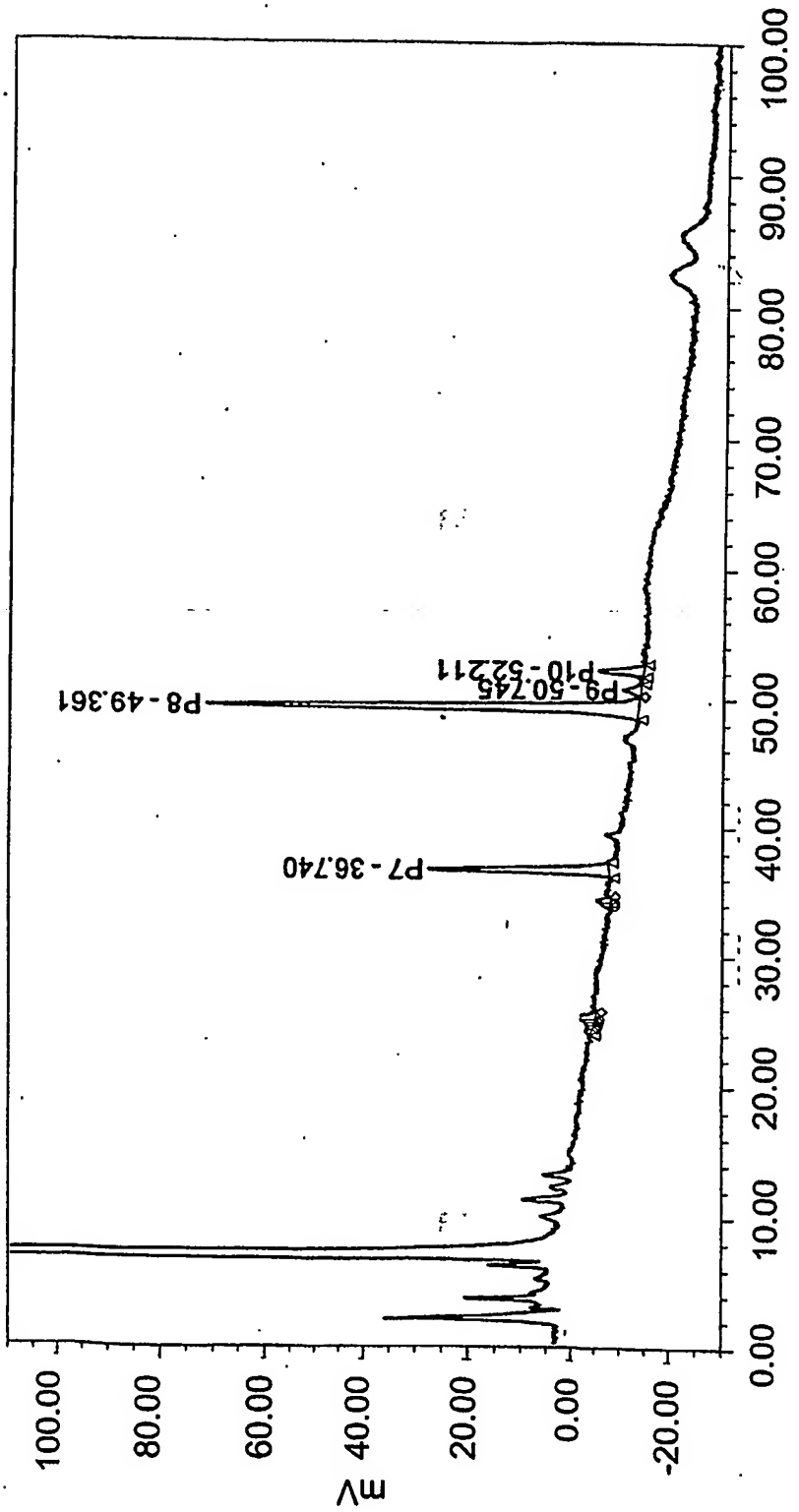
mV
100.00
80.00
60.00
40.00
20.00
0.00
-20.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
100.00
Minutes
P8 - 49.361
P9 - 50.745
P10 - 52.211
P7 - 36.740

FIG. 113C

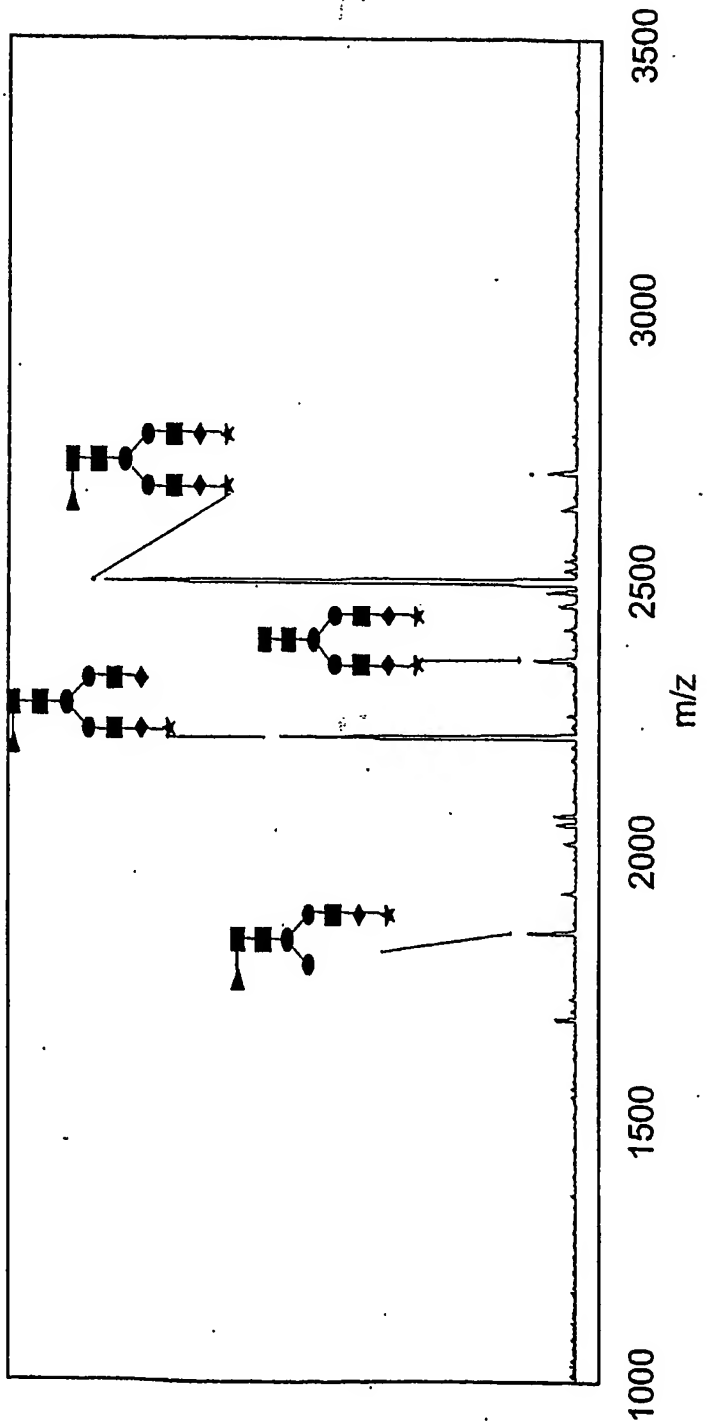

FIG. 114A

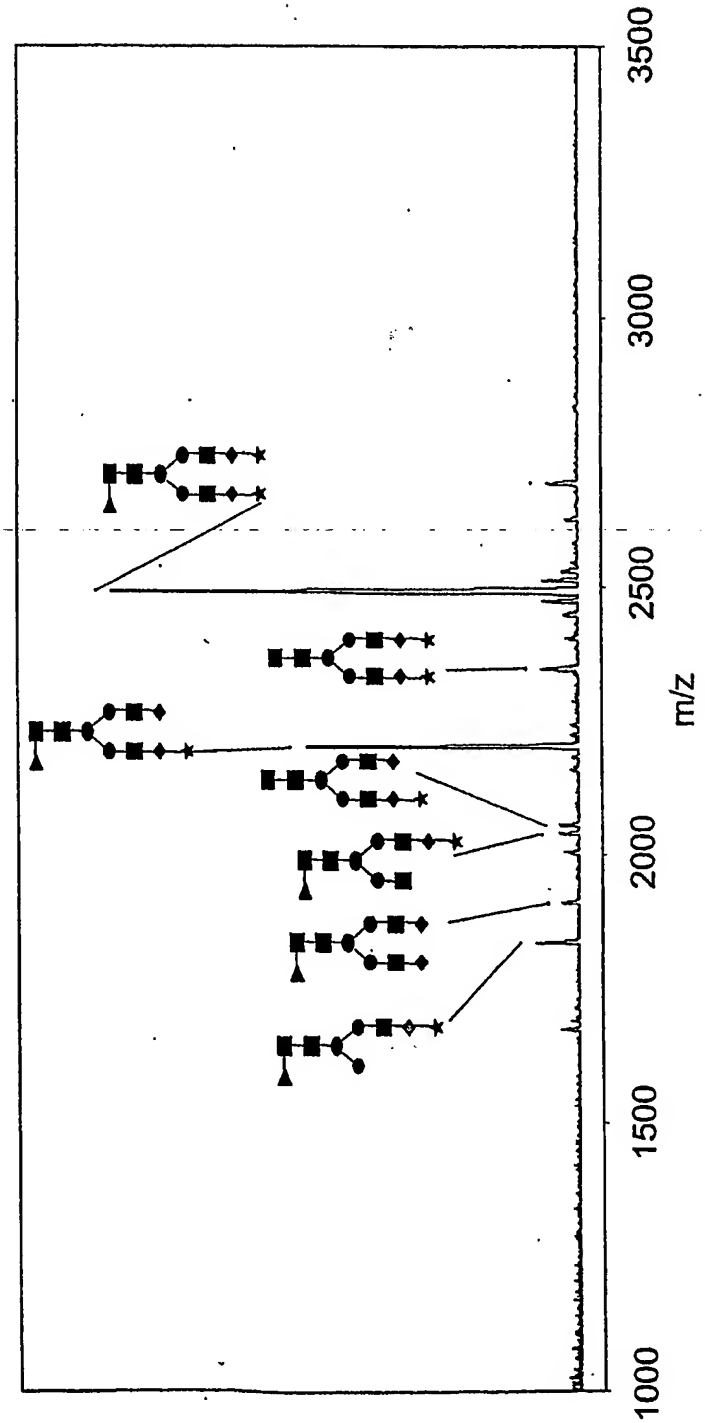

FIG. 114B

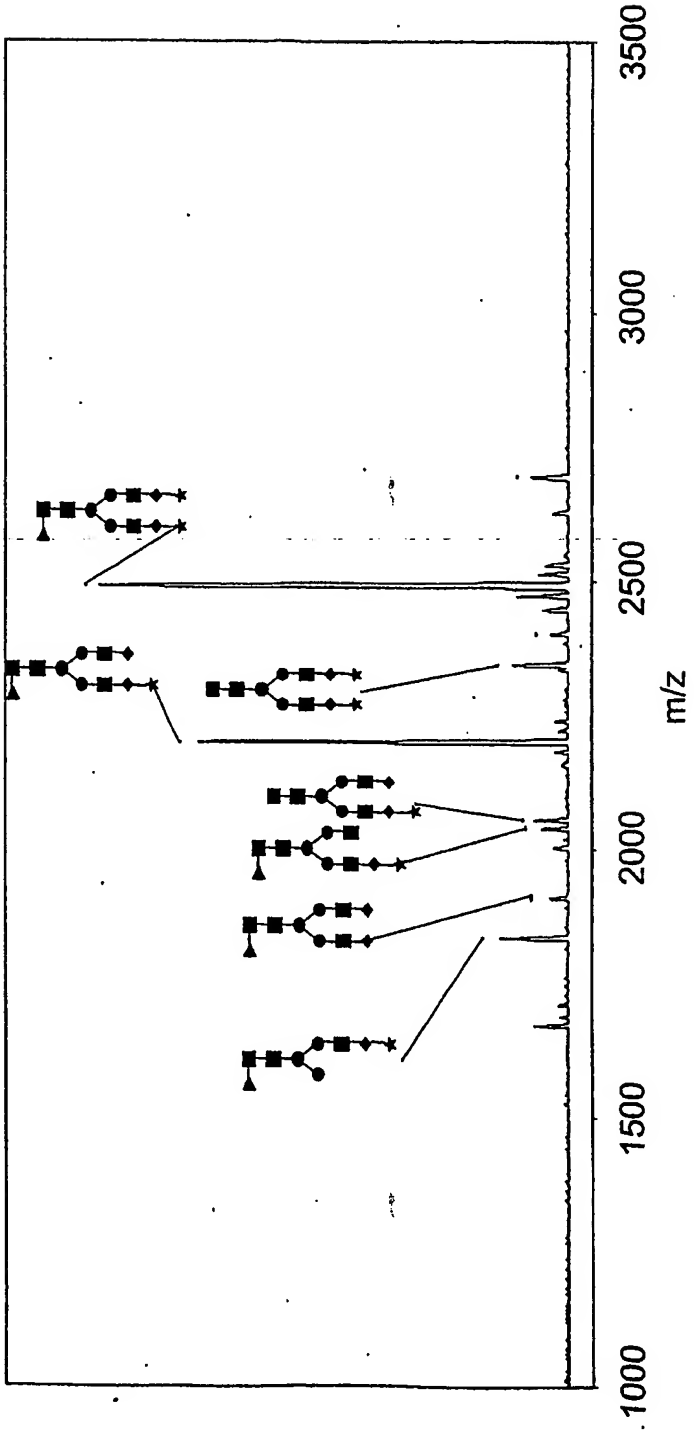

FIG. 114C

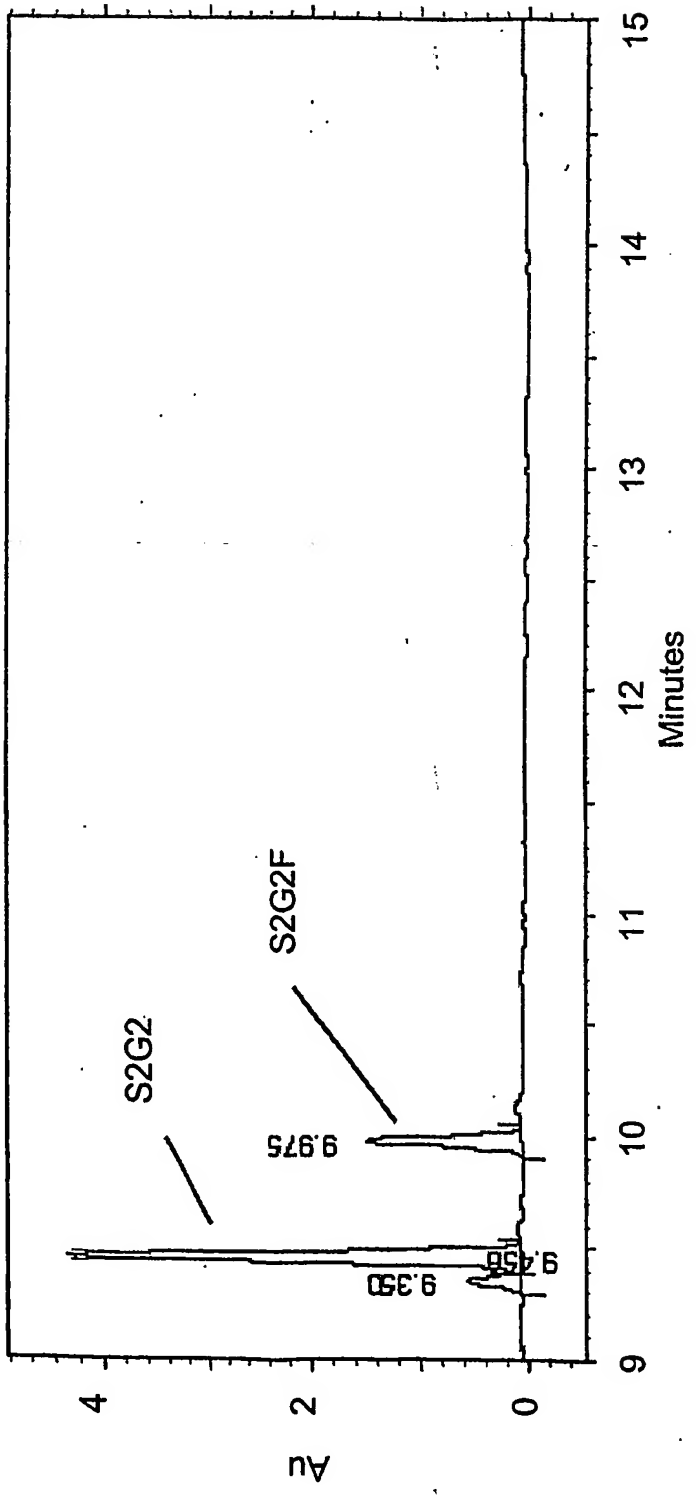

FIG. 115A

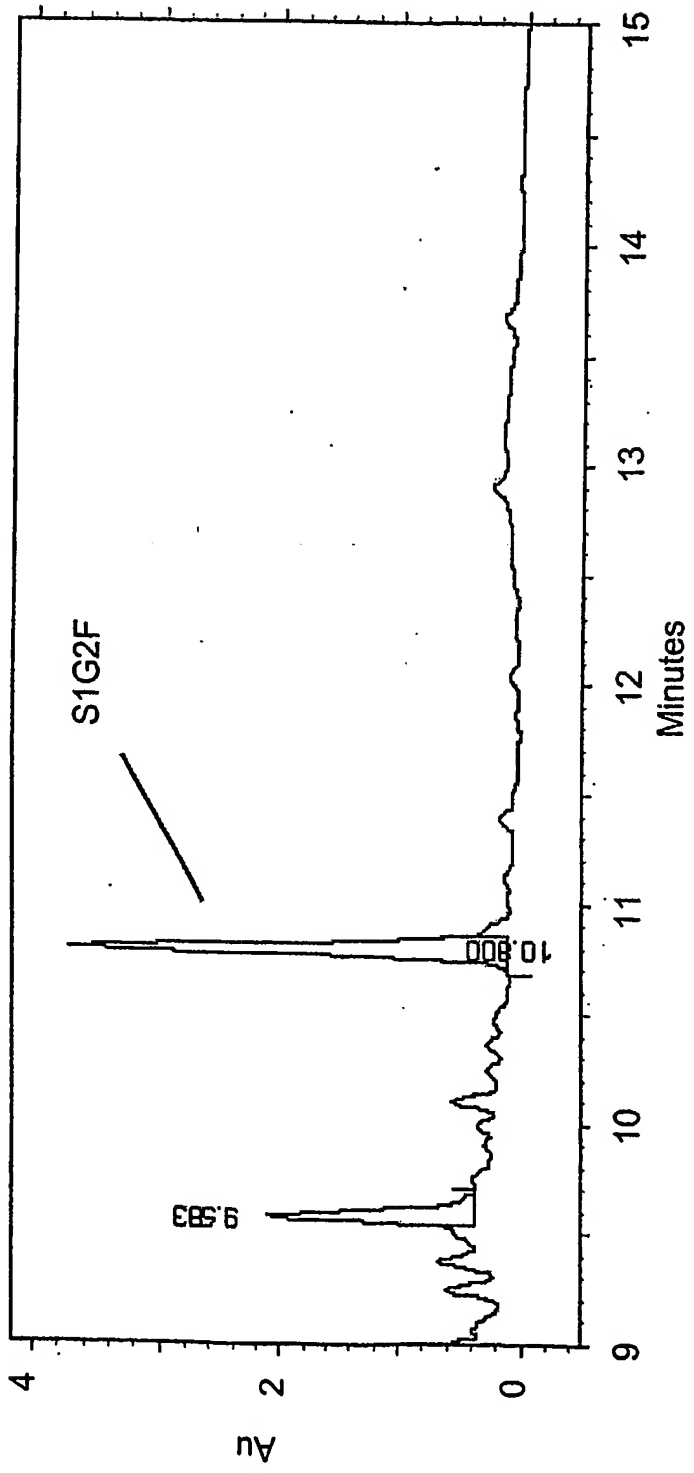

FIG. 115B

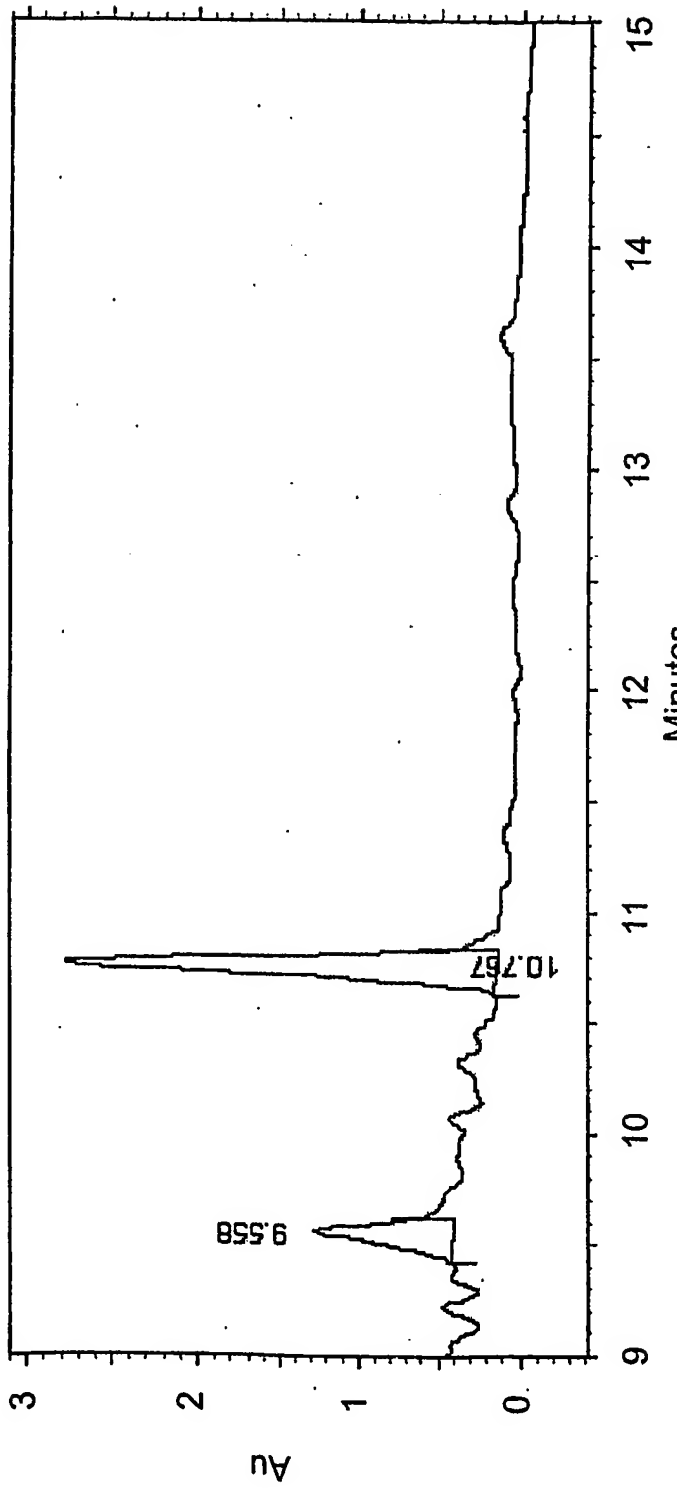

FIG. 115C

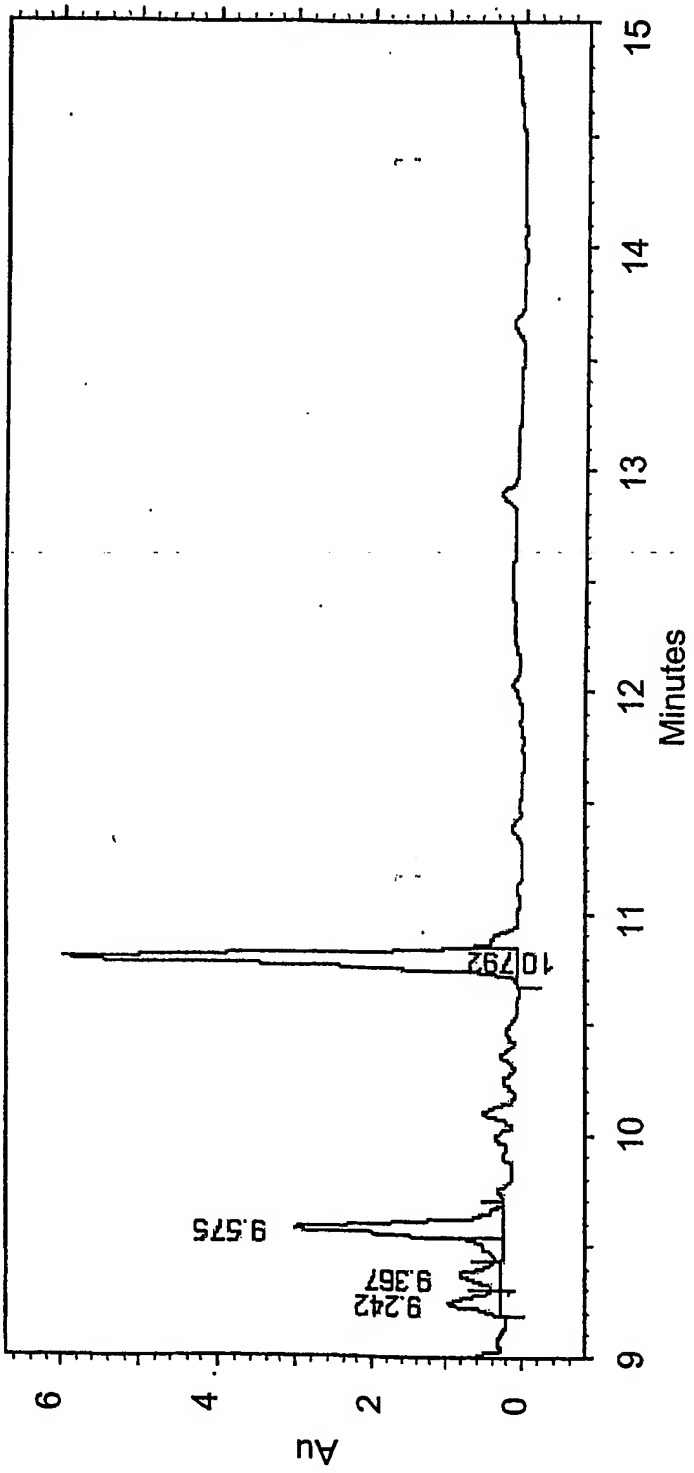

FIG. 115D

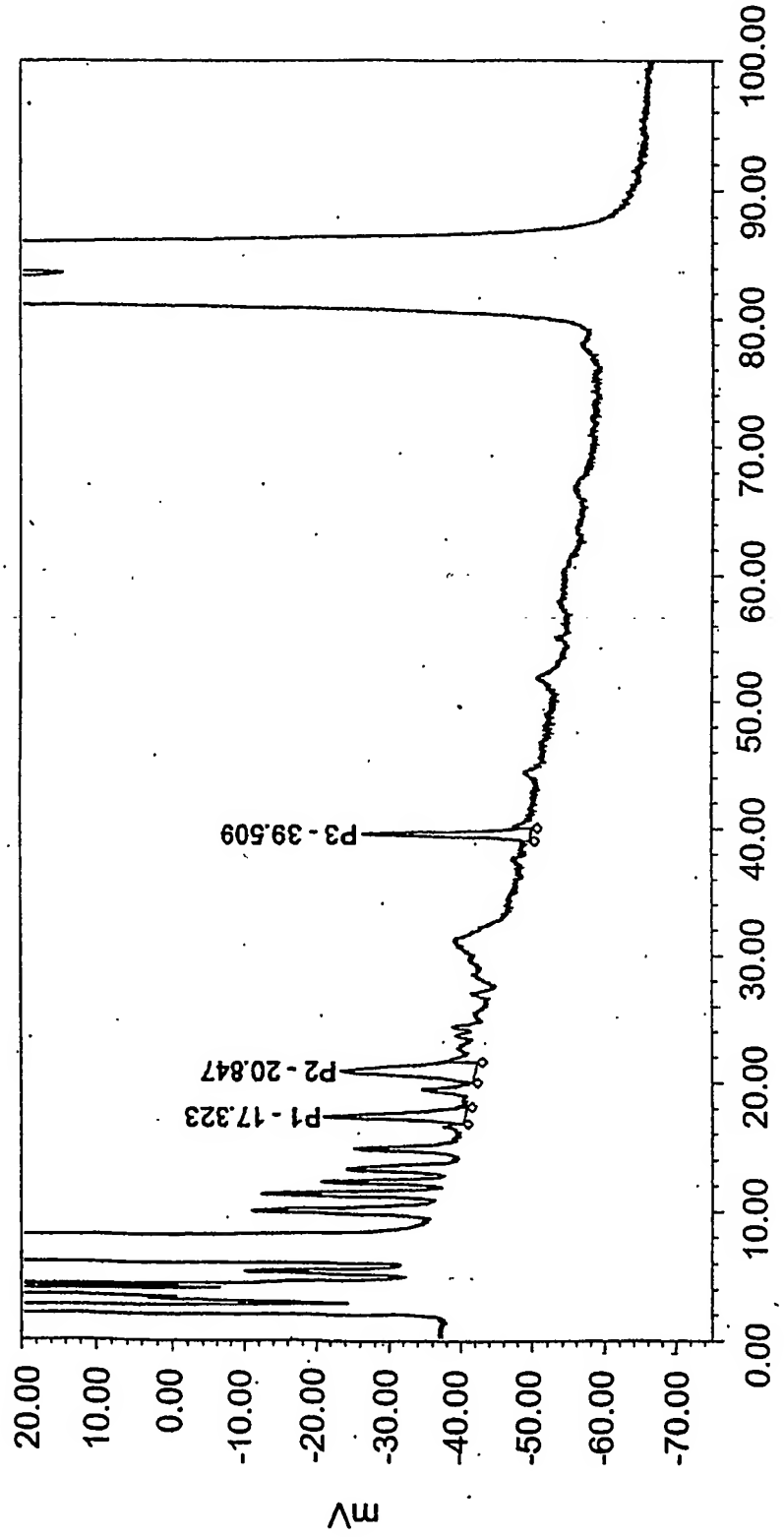
mV
20.00
10.00
0.00
-10.00
-20.00
-30.00
-40.00
-50.00
-60.00
-70.00
Minutes
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
100.00
P3 - 39.509
P2 - 20.847
P1 - 17.323

FIG. 116A

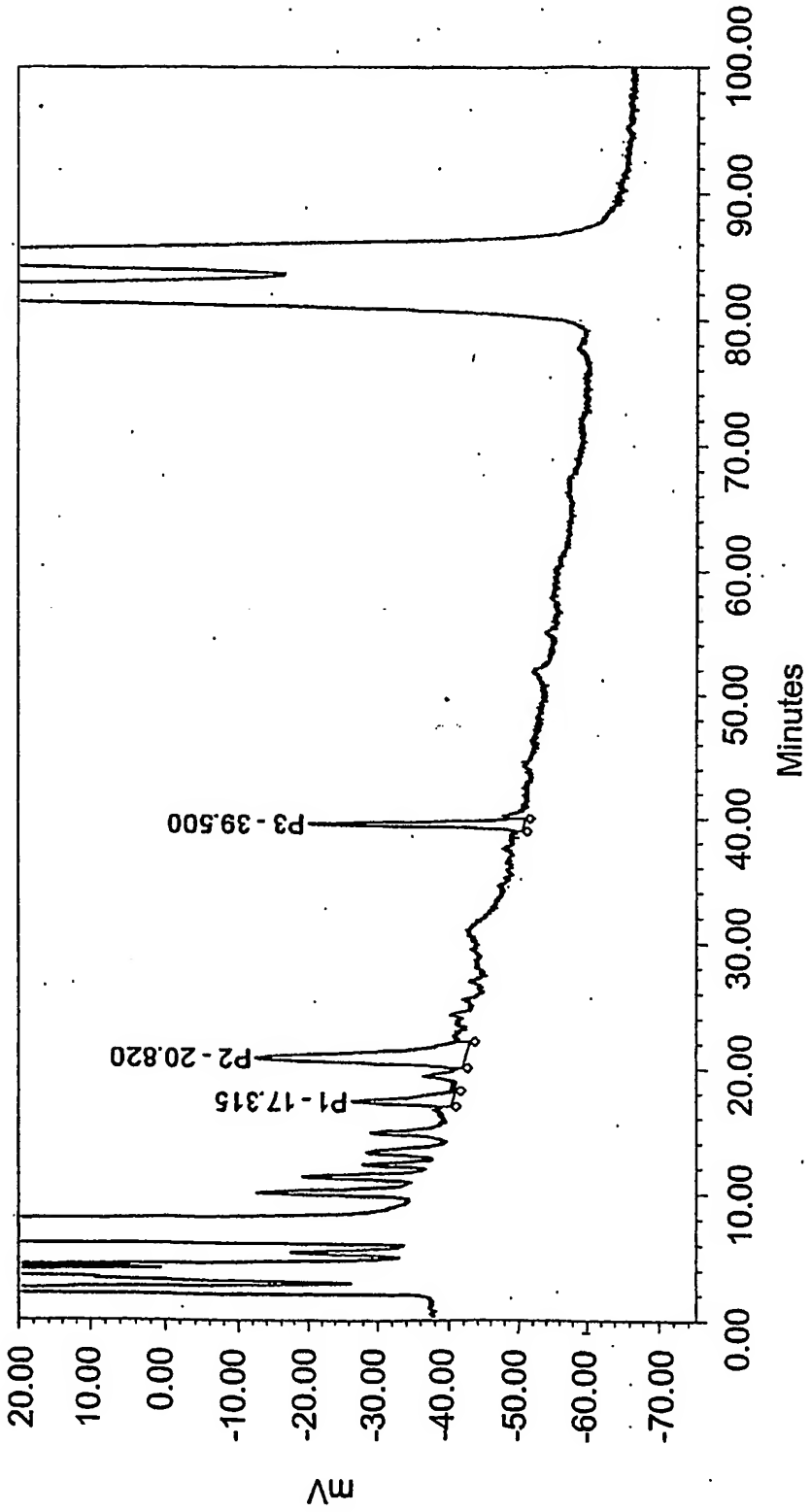
mV
20.00
10.00
0.00
-10.00
-20.00
-30.00
-40.00
-50.00
-60.00
-70.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
100.00
Minutes
P3 - 39.500
P2 - 20.820
P1 - 17.315

FIG. 116B

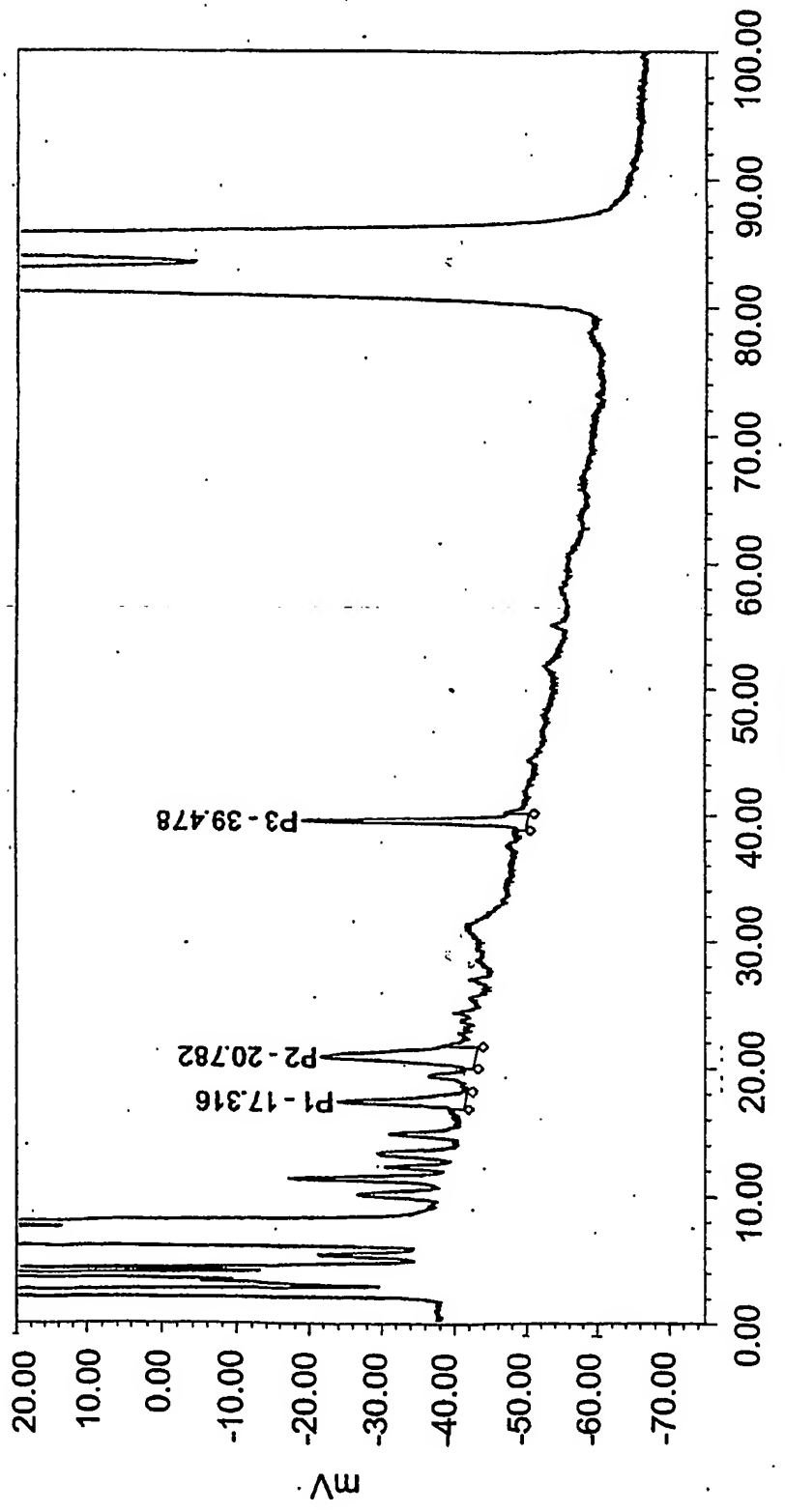
mV
20.00
10.00
0.00
-10.00
-20.00
-30.00
-40.00
-50.00
-60.00
-70.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
100.00
Minutes
P3 - 39.478
P2 - 20.782
P1 - 17.316

FIG. 116C

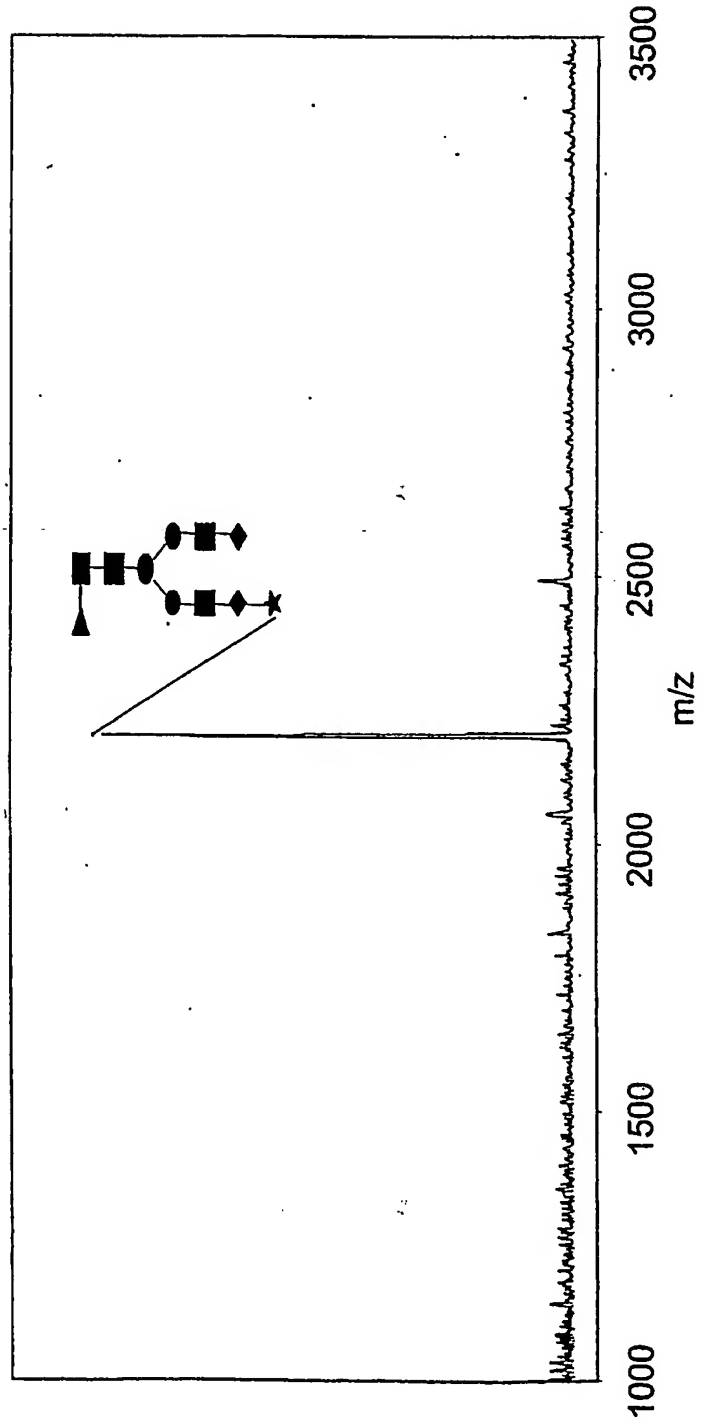

FIG. 117A

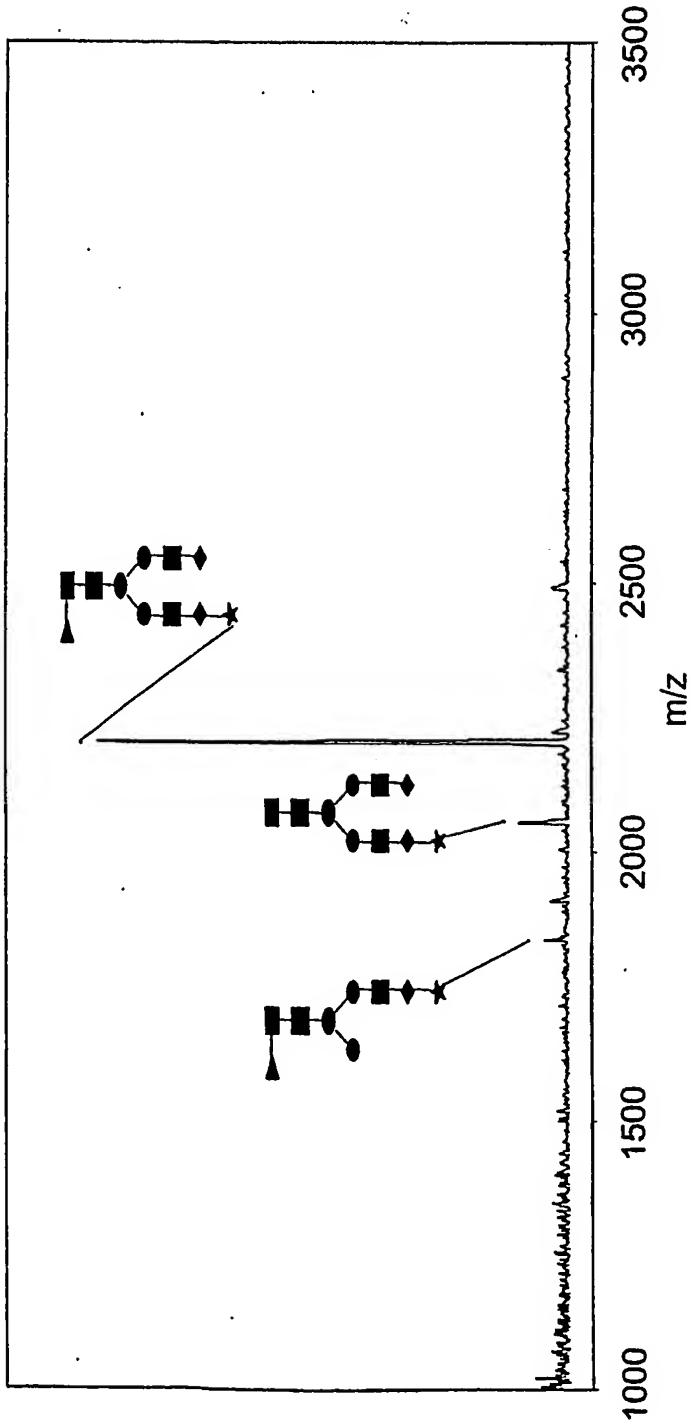

FIG. 117B

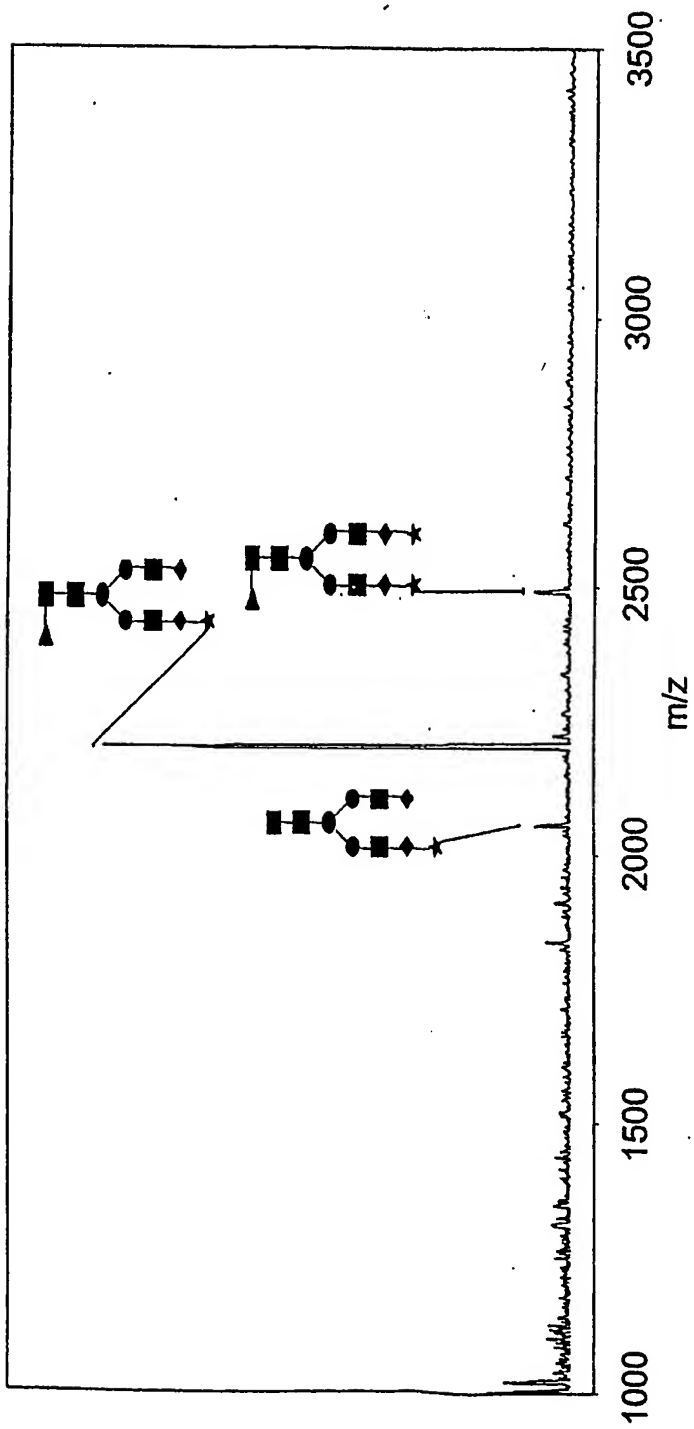

FIG. 117C

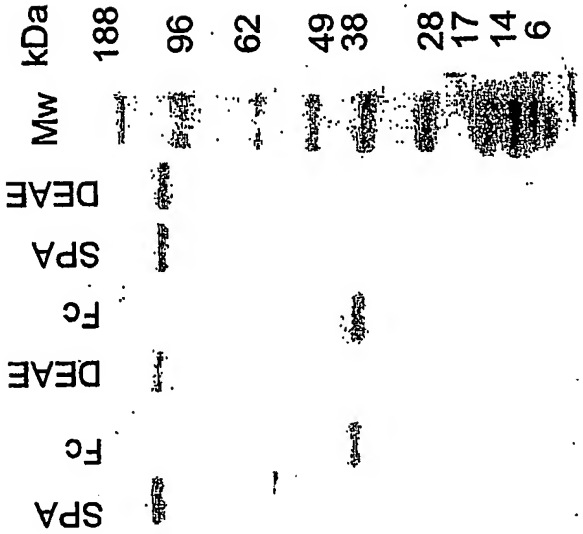

FIG. 118B

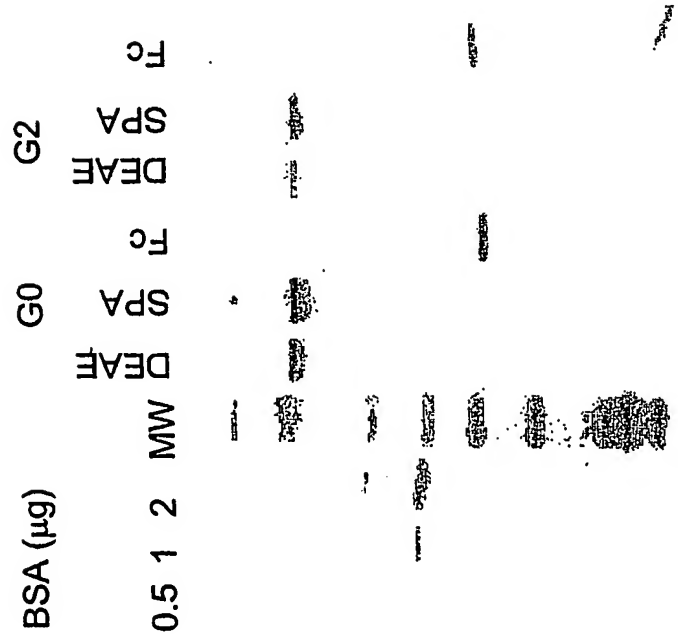

FIG. 118A

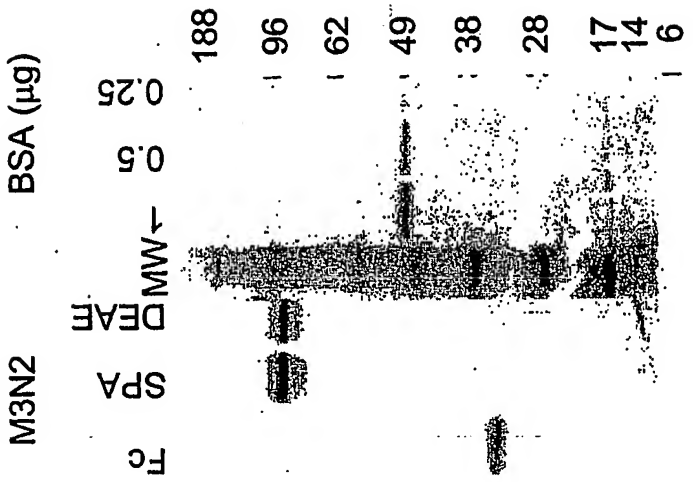

FIG. 118D

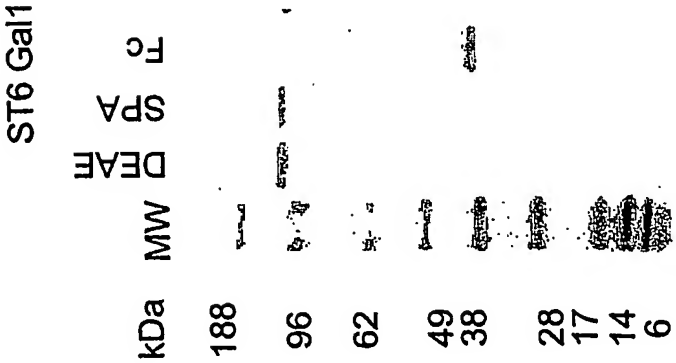

FIG. 118C

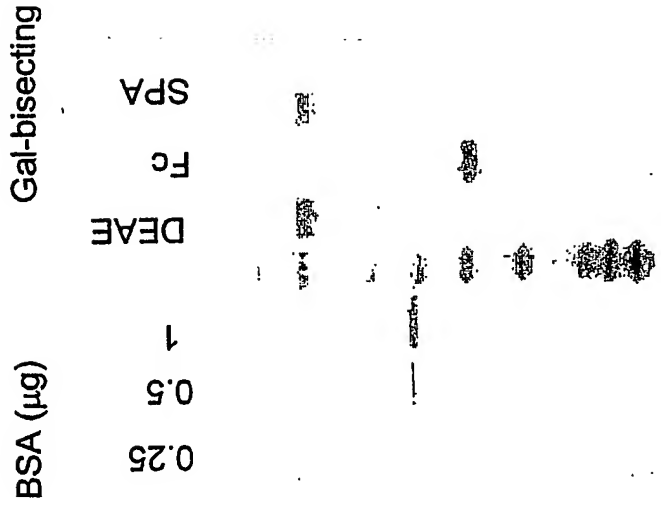

FIG. 118E

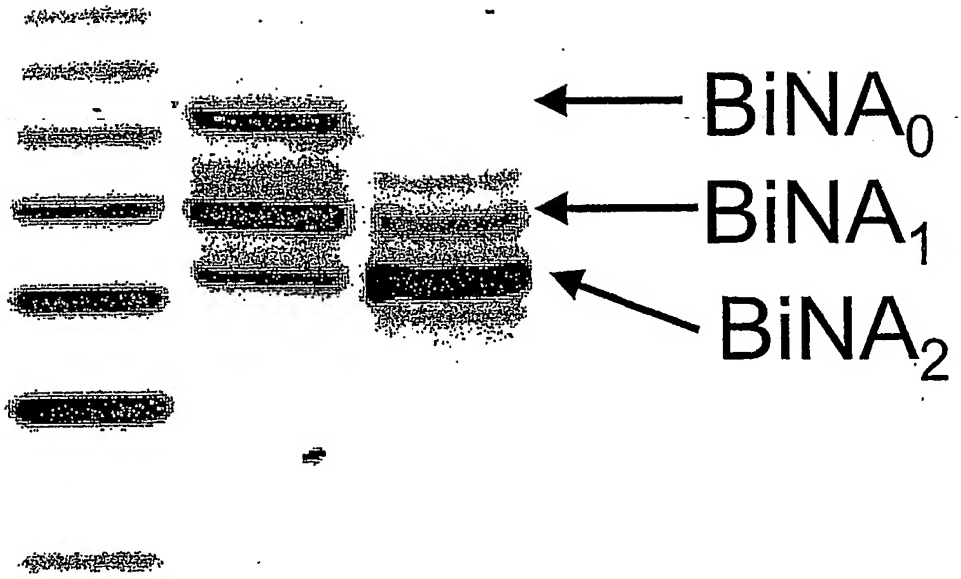

FIG. 119

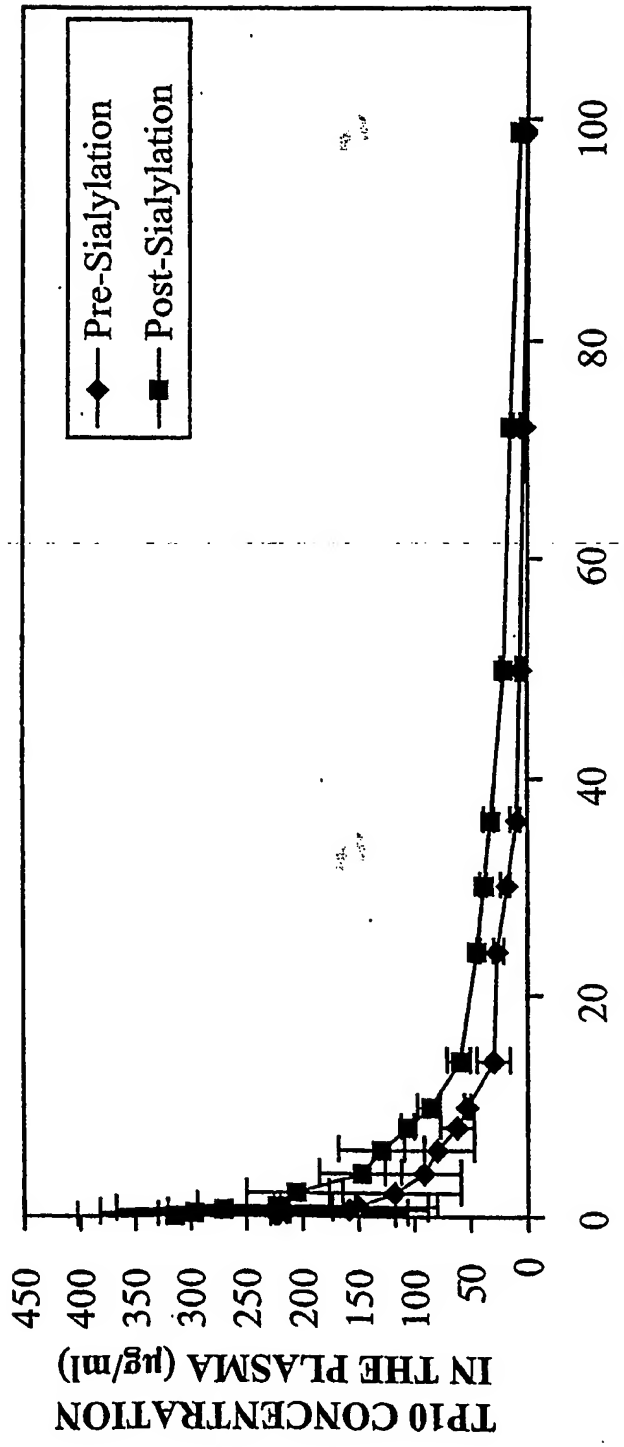
Pre-Sialylation
Post-Sialylation
TP10 CONCENTRATION IN THE PLASMA (μg/ml)
450
400
350
300
250
200
150
100
50
0
0
20
40
60
80
100
HOURS

FIG. 120

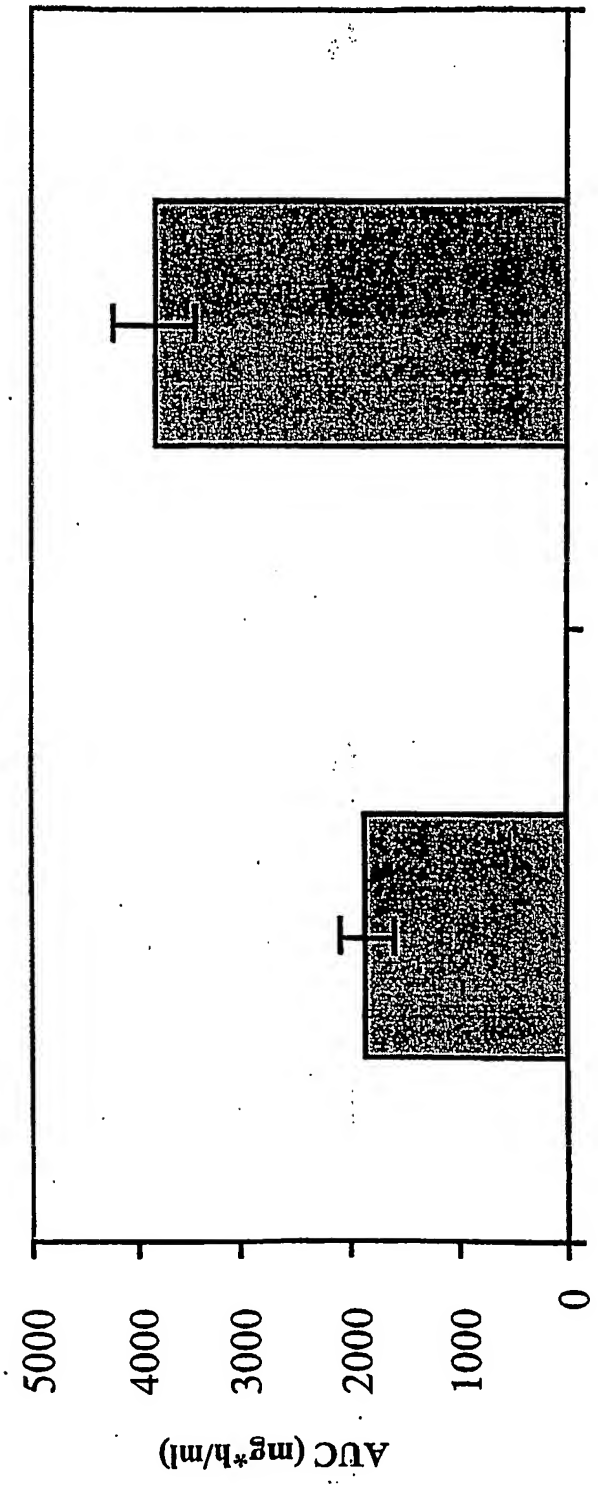
AUC (mg*h/ml)
5000
4000
3000
2000
1000
0
Pre-Sialylation
Post-Sialylation

FIG. 121

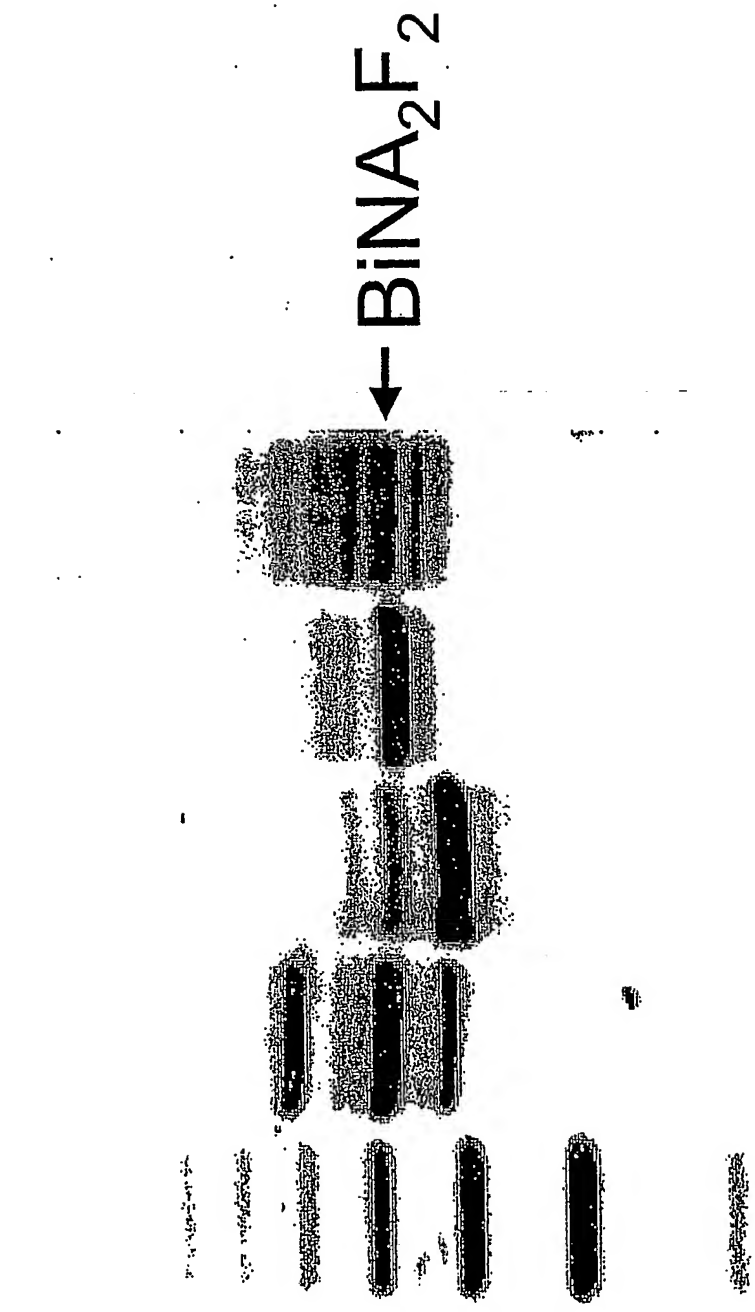

FIG. 122

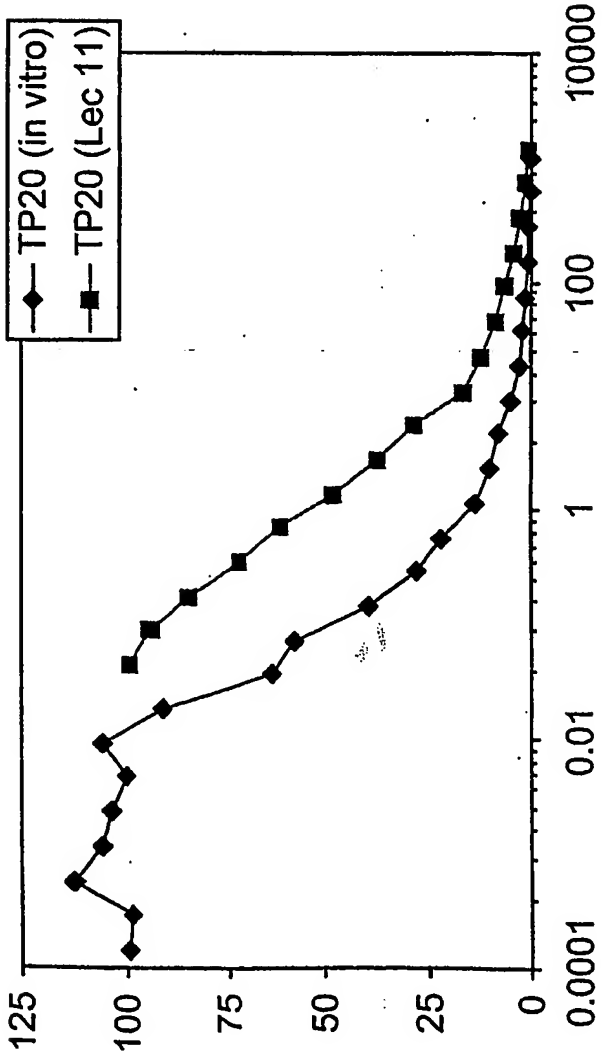
TP20 (in vitro)
TP20 (Lec 11)
125
100
75
50
25
0
0.0001
0.01
1
100
10000
µg/mL TP20

FIG. 123

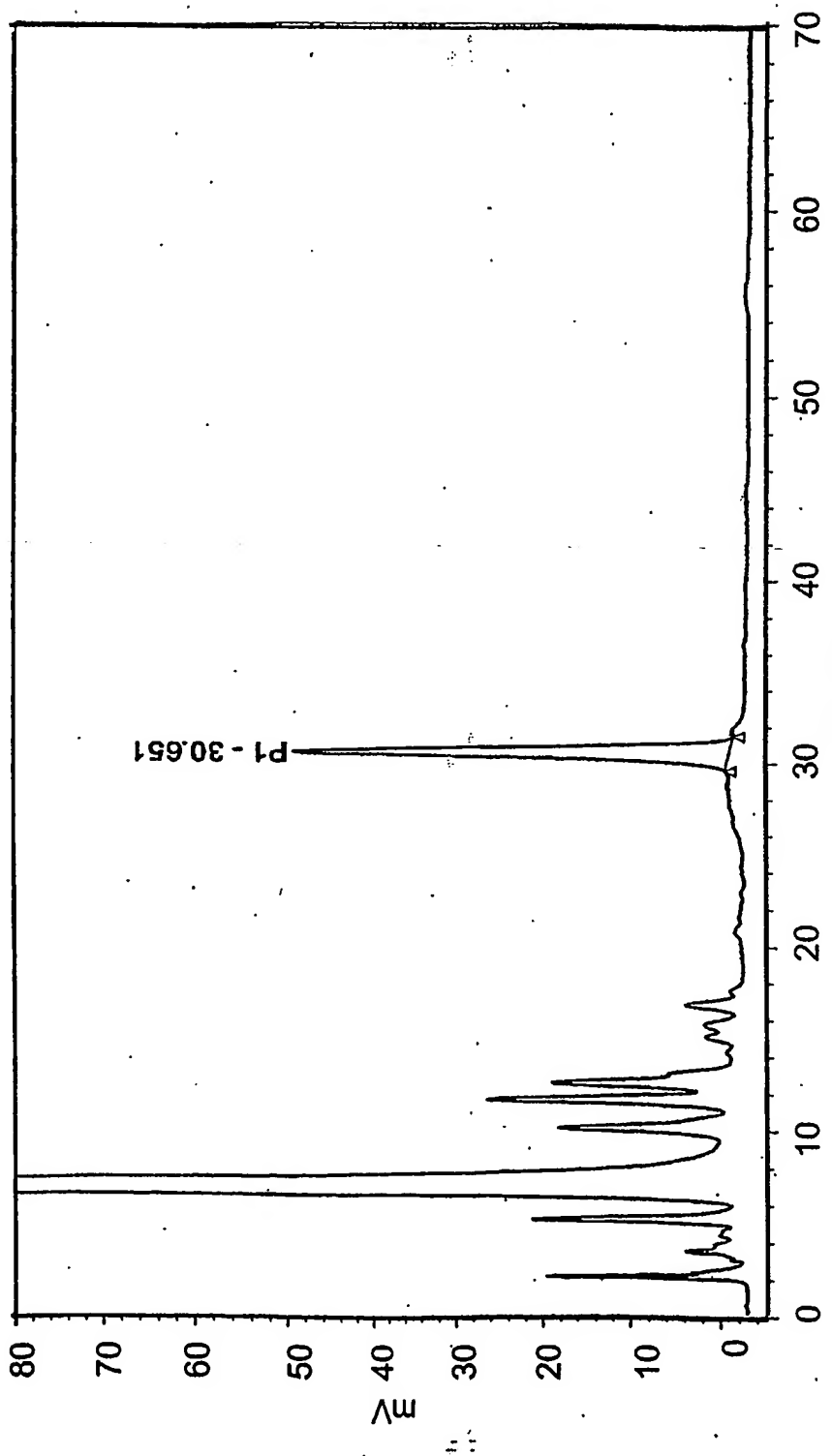

FIG. 124

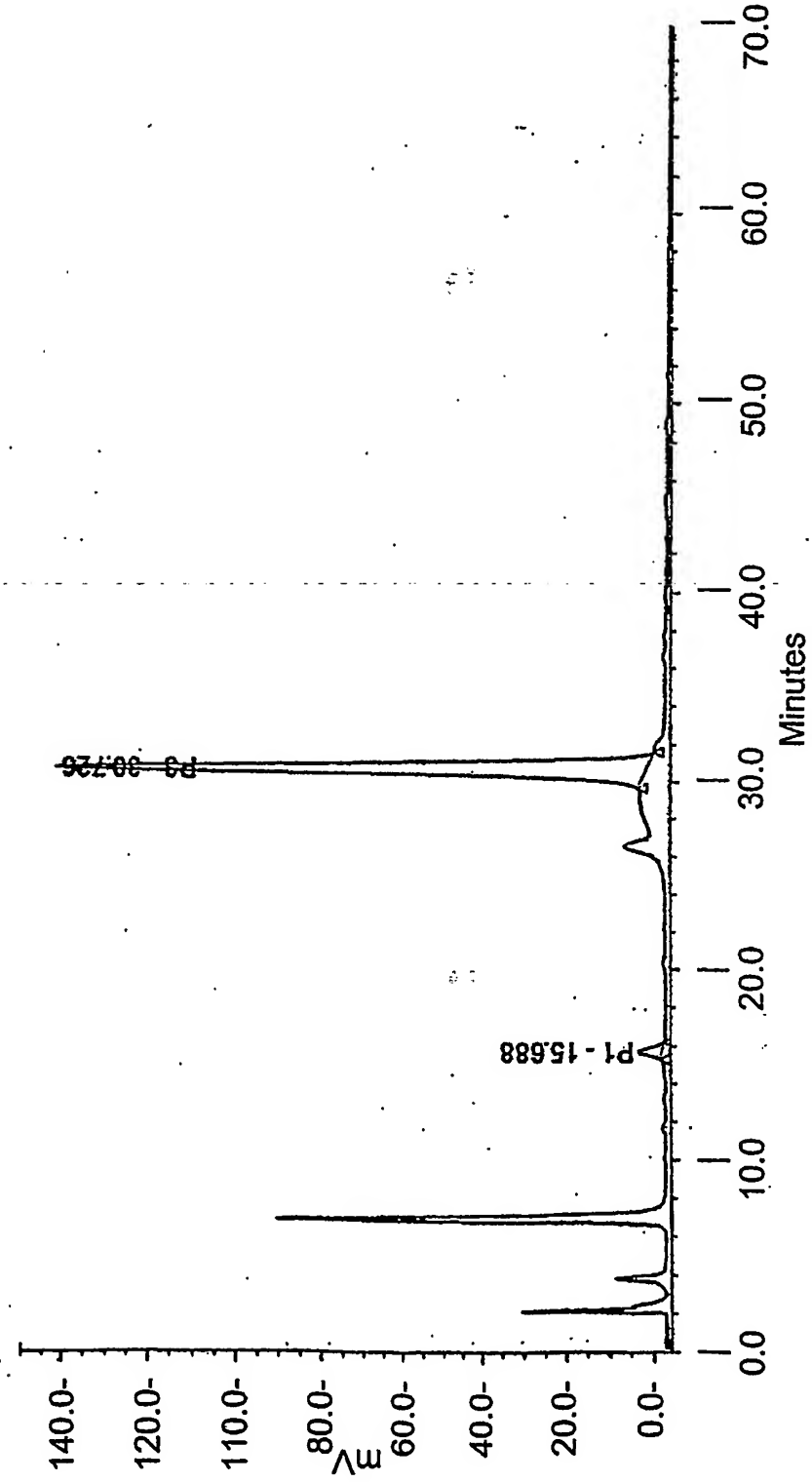
mV
140.0-
120.0-
110.0-
80.0-
60.0-
40.0-
20.0-
0.0-
0.0
10.0
20.0
30.0
40.0
50.0
60.0
70.0
Minutes
P1 - 15.688
P3 - 30.726

FIG. 125A

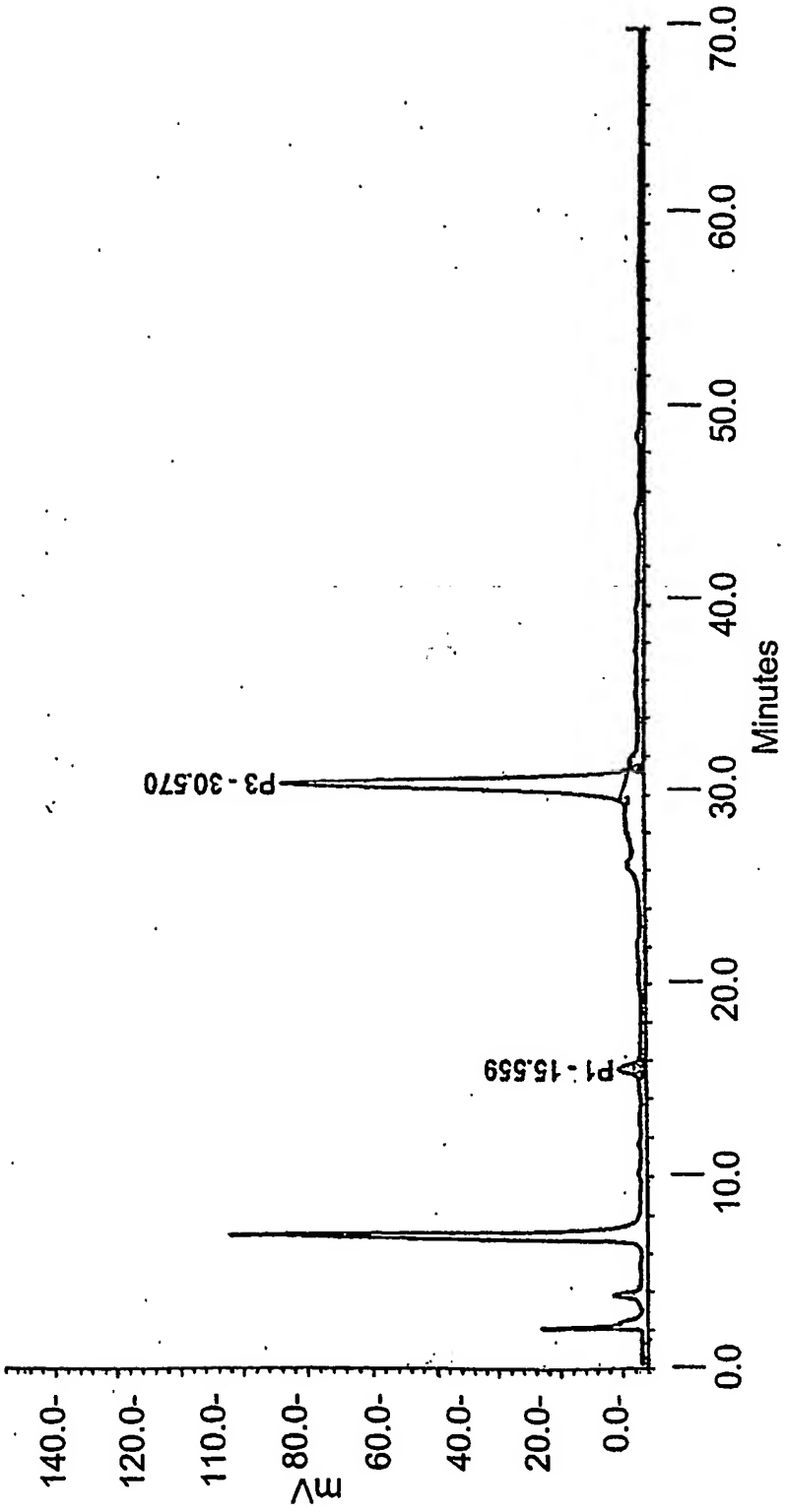
mV
140.0-
120.0-
110.0-
80.0-
60.0-
40.0-
20.0-
0.0-
0.0
10.0
20.0
30.0
40.0
50.0
60.0
70.0
Minutes
P1 - 15.559
P3 - 30.570

FIG. 125B

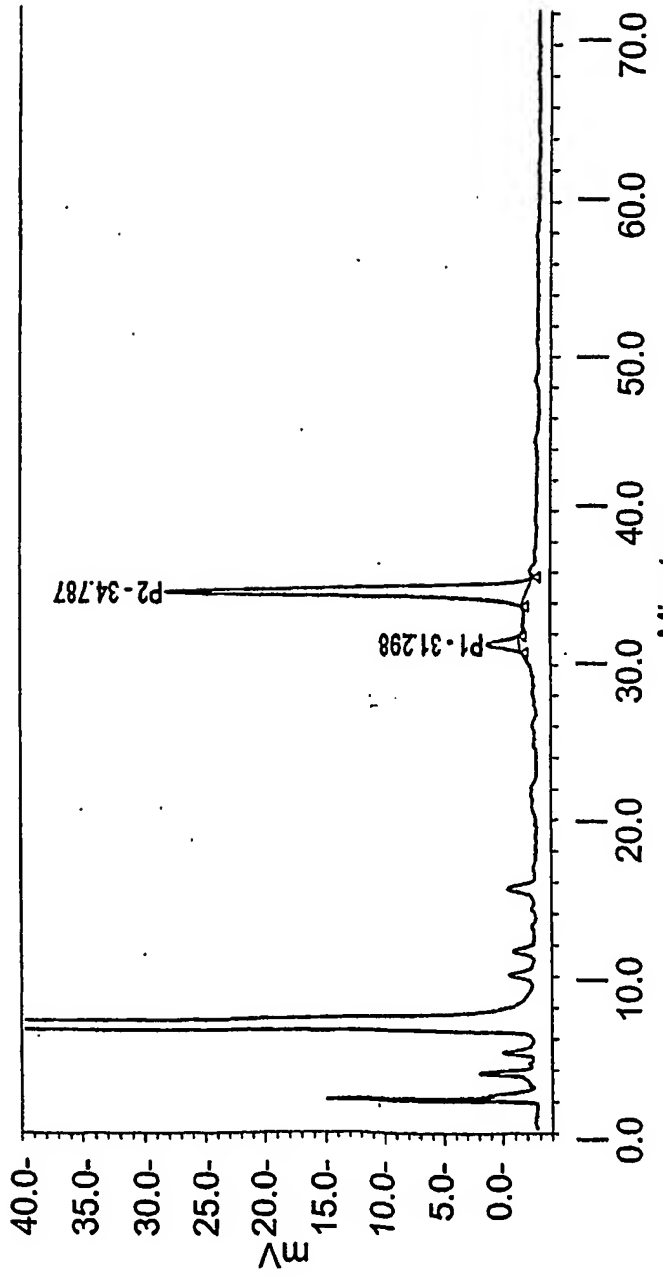
40.0-
35.0-
30.0-
25.0-
20.0-
15.0-
10.0-
5.0-
0.0-
mV
0.0
10.0
20.0
30.0
40.0
50.0
60.0
70.0
Minutes
P1-31.298
P2-34.787

FIG. 126

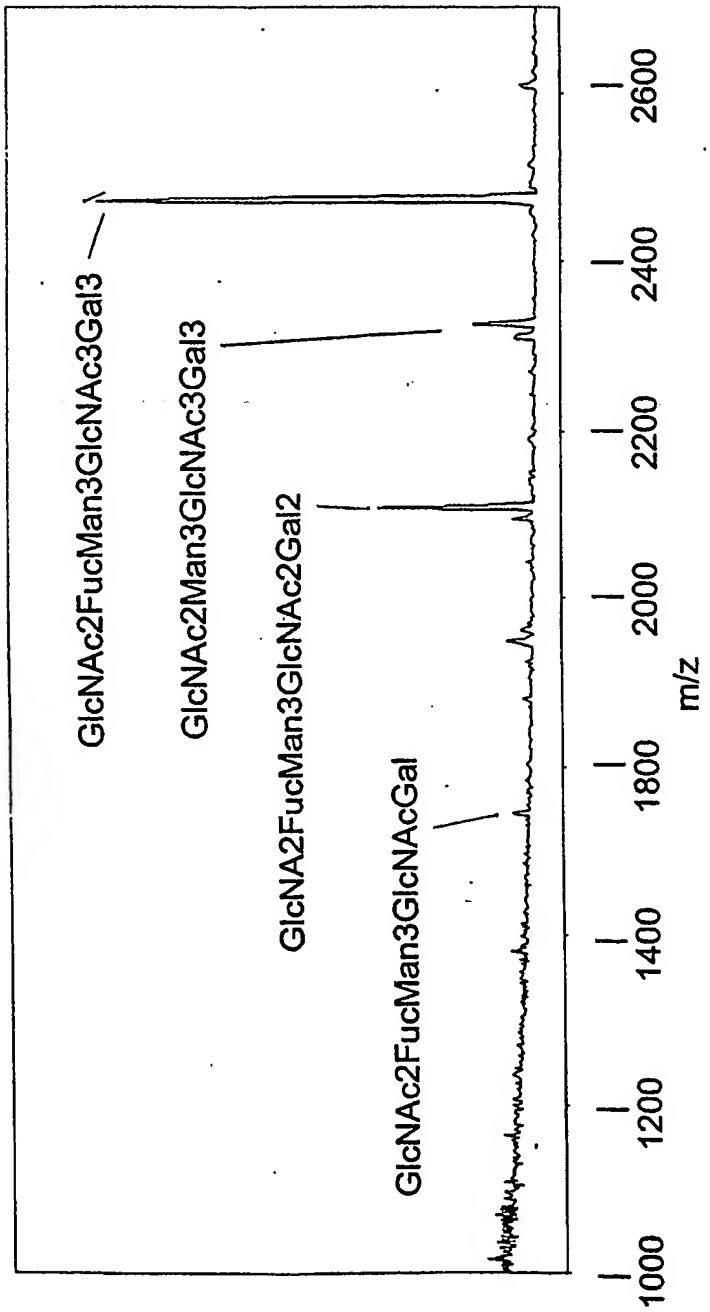
GlcNAc2FucMan3GlcNAc3Gal3
GlcNAc2Man3GlcNAc3Gal3
GlcNA2FucMan3GlcNAc2Gal2
GlcNAc2FucMan3GlcNAcGal
1000
1200
1400
1800
2000
2200
2400
2600
m/z

FIG. 127

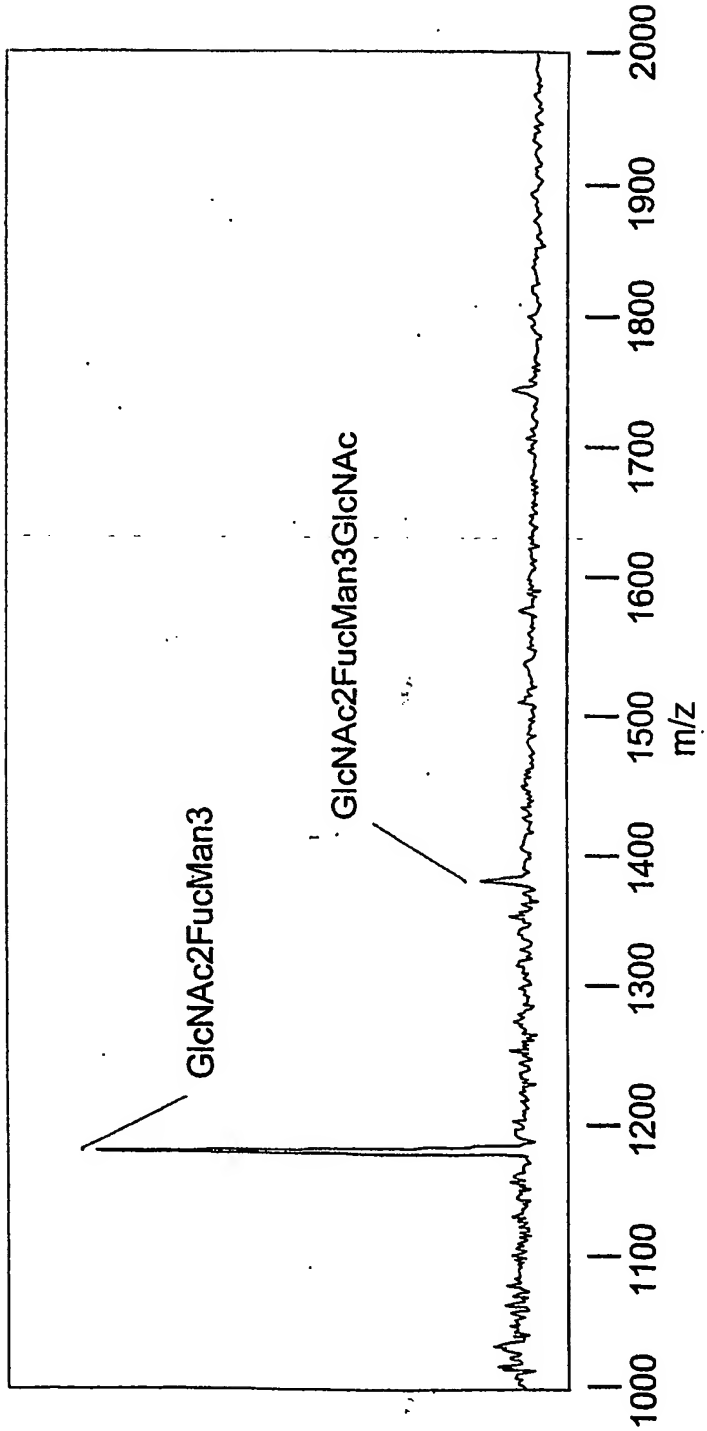
GlcNAc2FucMan3
GlcNAc2FucMan3GlcNAc
1000
1100
1200
1300
1400
1500
1600
1700
1800
1900
2000
m/z

FIG. 128

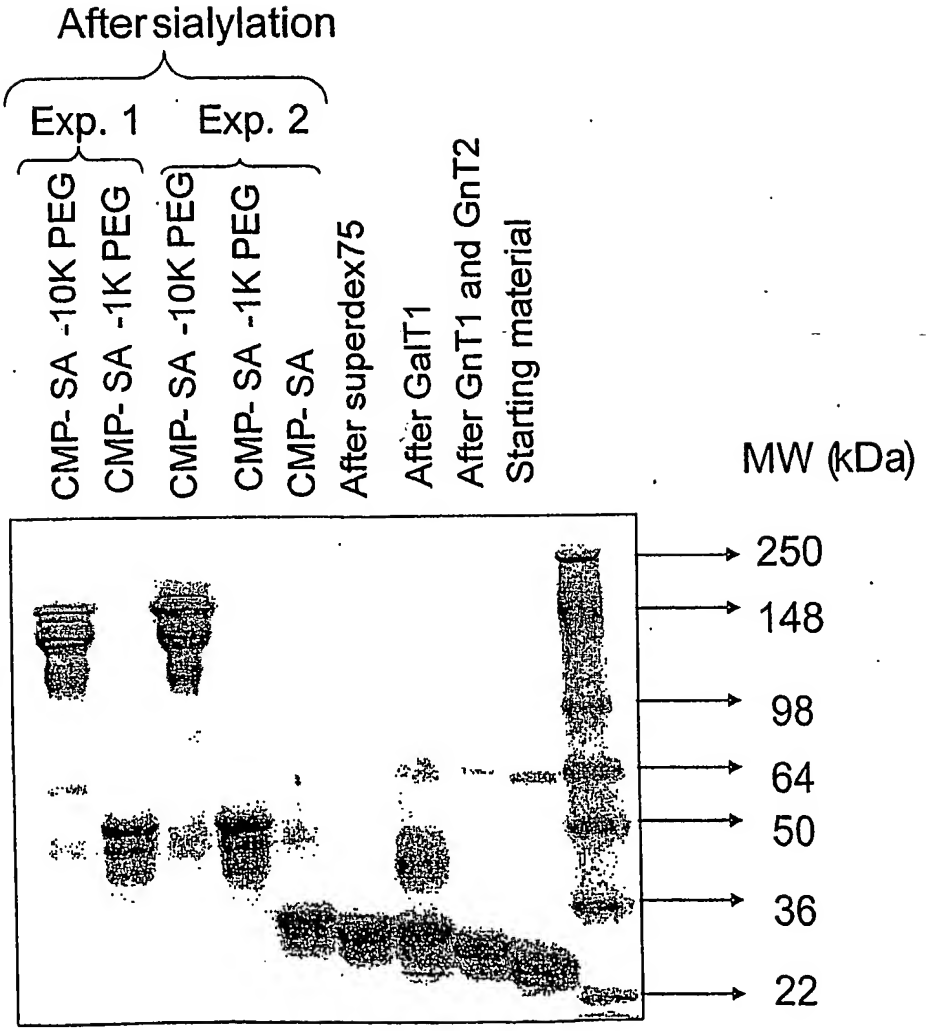
After sialylation
Exp. 1
Exp. 2
CMP- SA -10K PEG
CMP- SA -1K PEG
CMP- SA -10K PEG
CMP- SA -1K PEG
CMP- SA
After superdex75
After GalT1
After GnT1 and GnT2
Starting material
MW (kDa)
250
148
98
64
50
36
22

FIG. 129

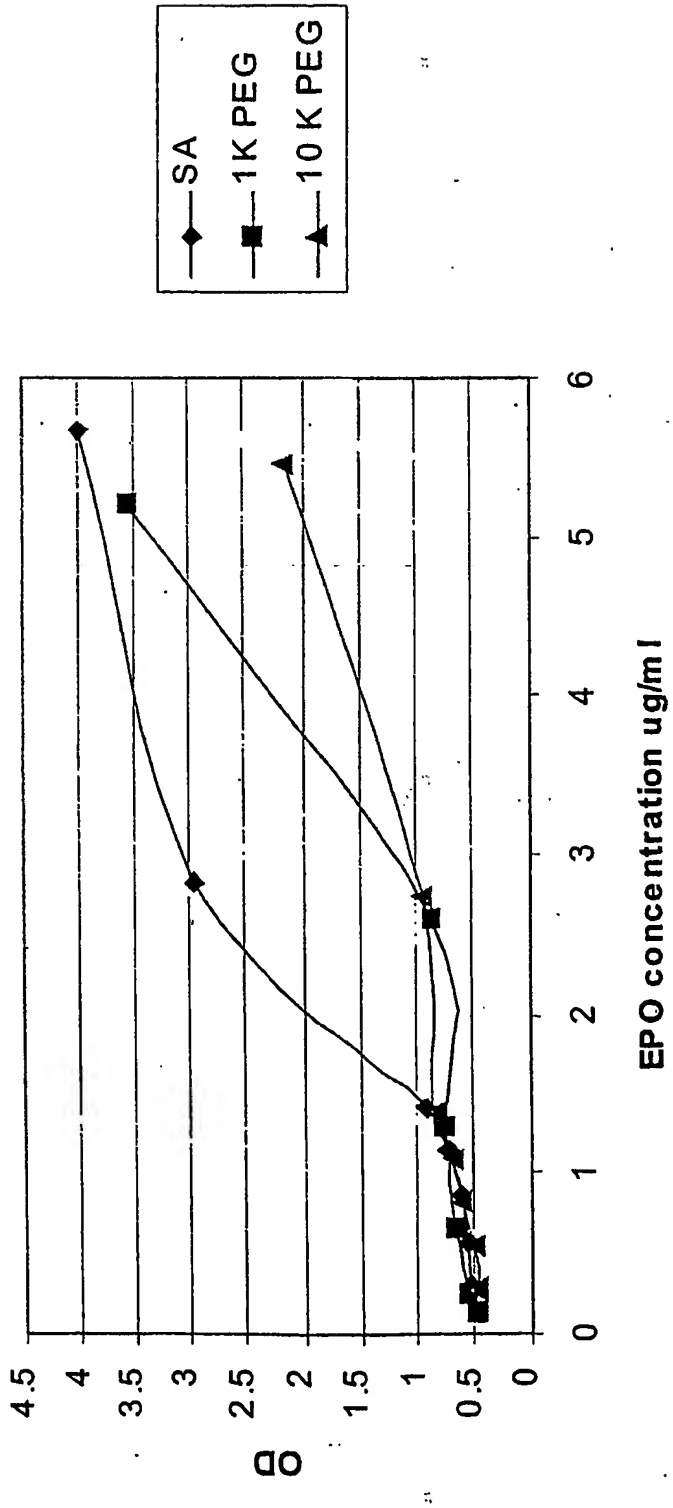
SA
1K PEG
10 K PEG
OD
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
0
1
2
3
4
5
6
EPO concentration ug/ml

FIG. 130

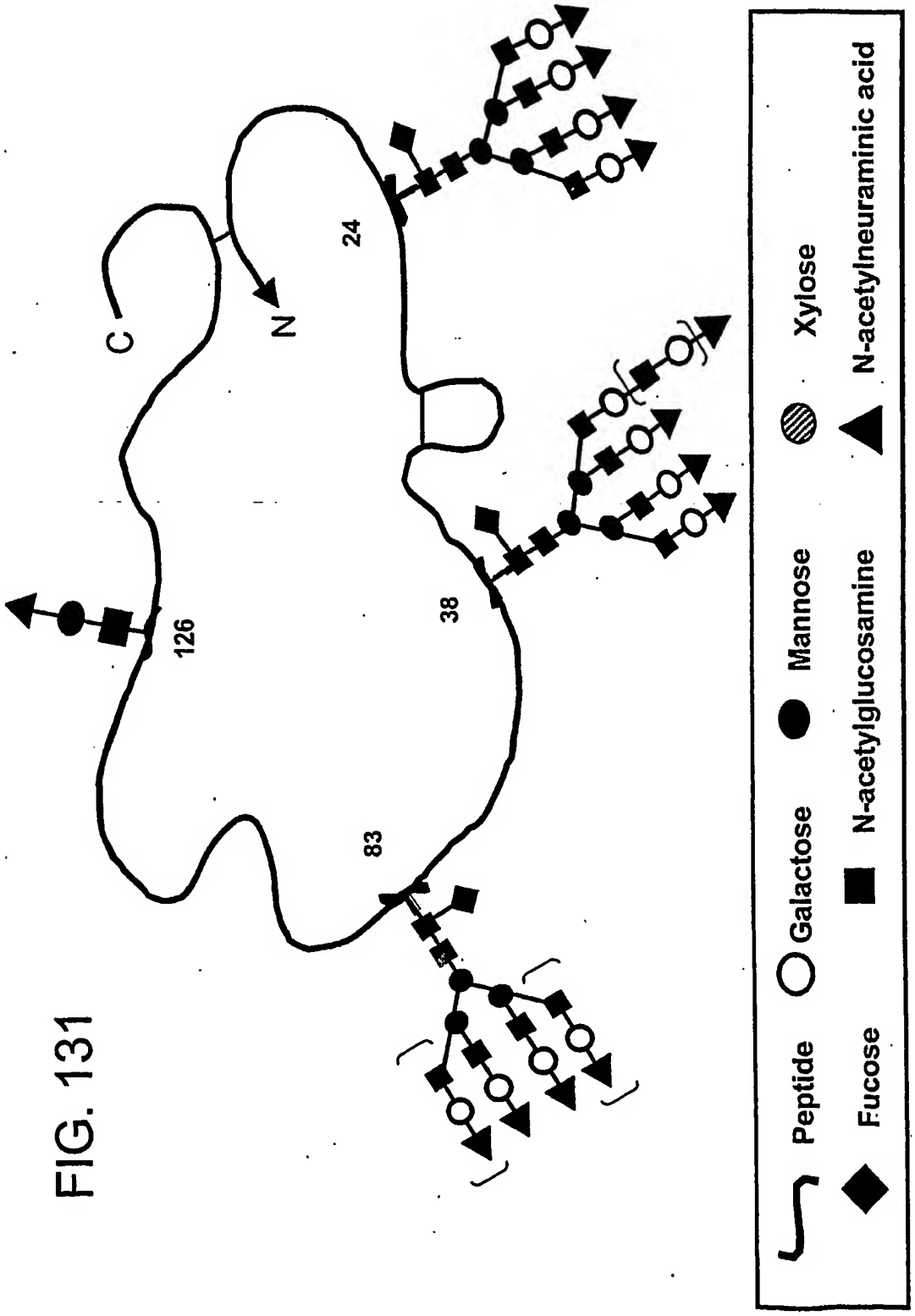
C
N
24
38
83
126
Peptide
Galactose
Mannose
Xylose
Fucose
N-acetylglucosamine
N-acetylneuraminic acid

FIG. 131

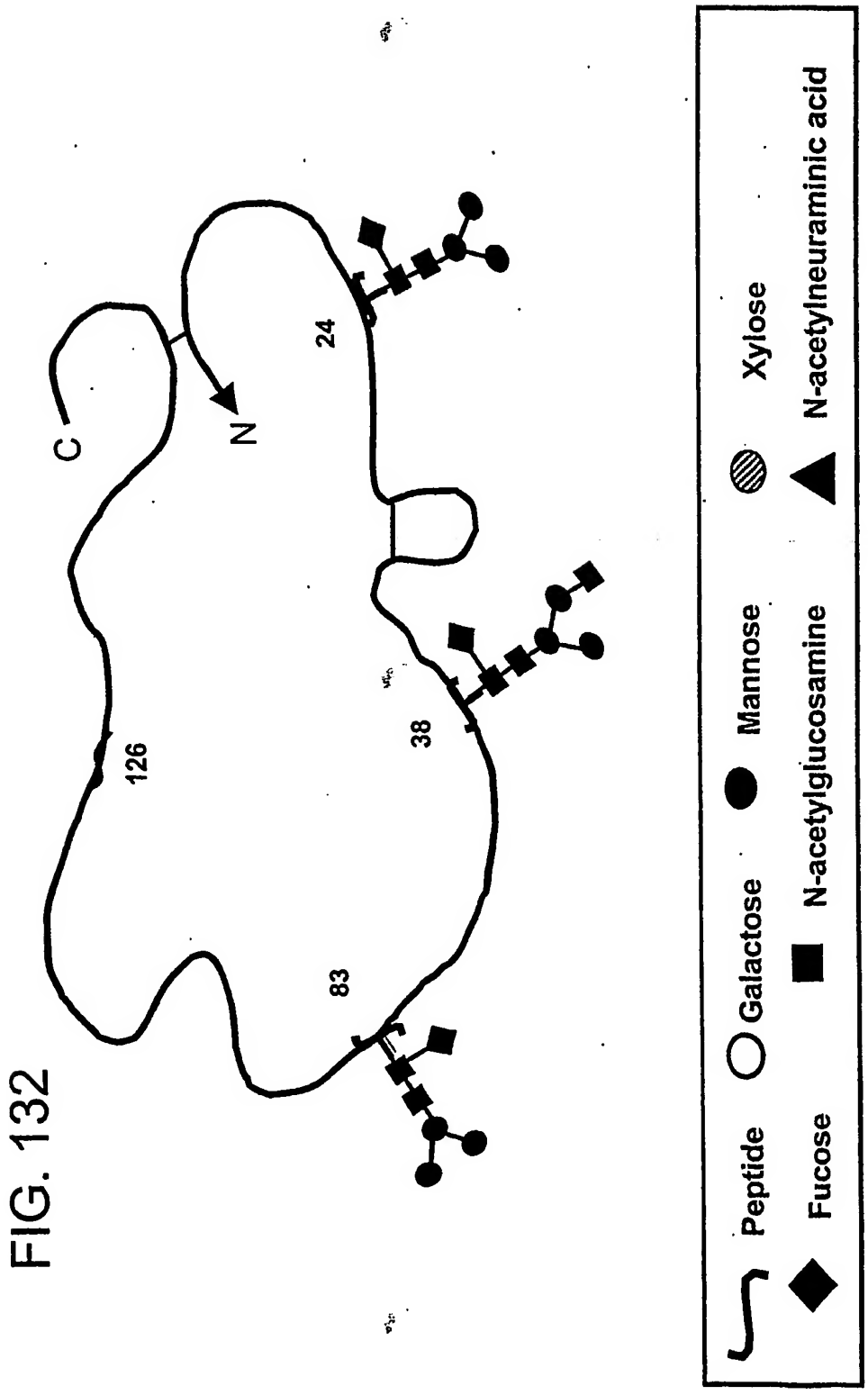
C
N
24
38
83
126
Peptide
Galactose
Mannose
Xylose
Fucose
N-acetylglucosamine
N-acetylneuraminic acid

FIG. 132

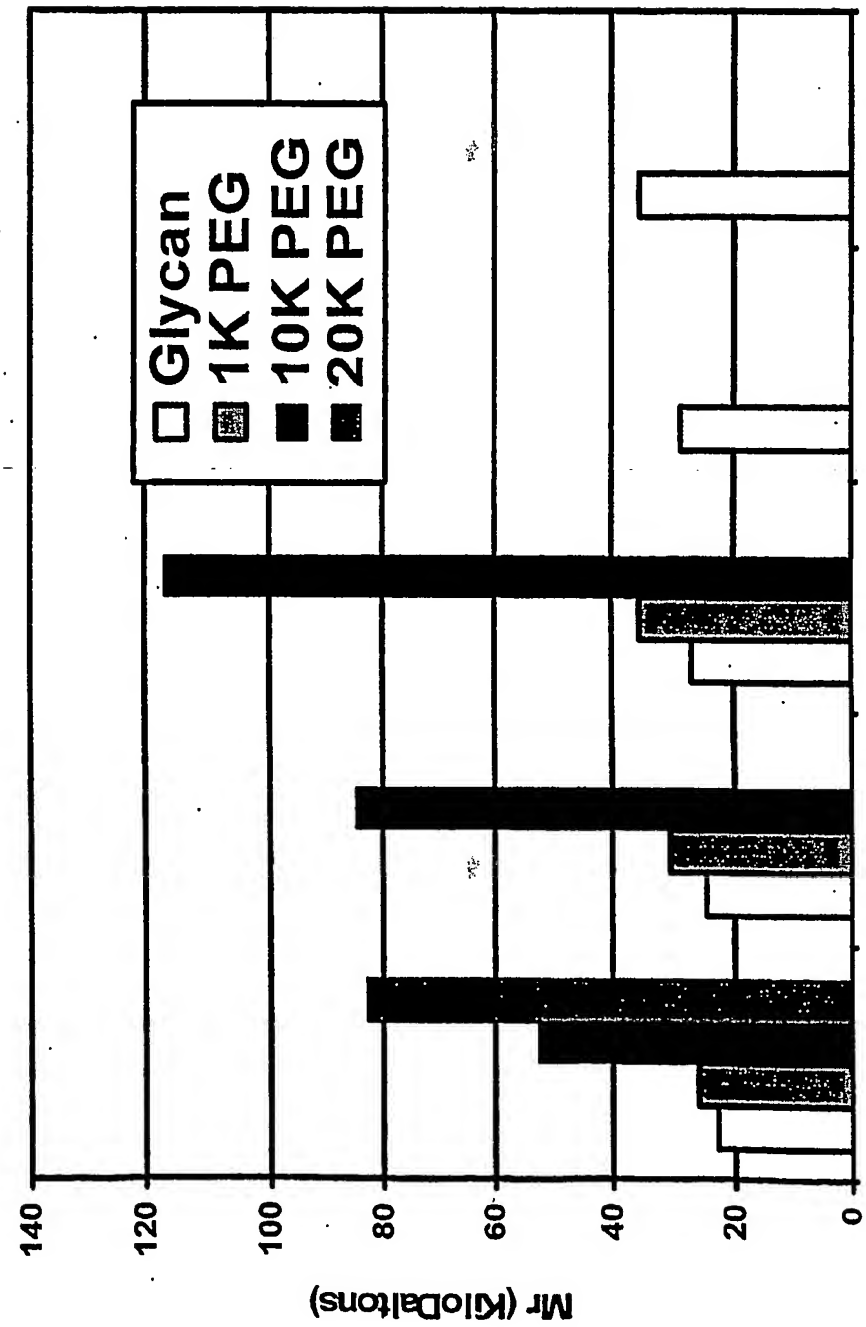
Glycan
1K PEG
10K PEG
20K PEG
Mr (KiloDaltons)
0
20
40
60
80
100
120
140
Monoantennary EPO
Biantennary EPO
Triantennary EPO
Epoetin
NESP

FIG. 133

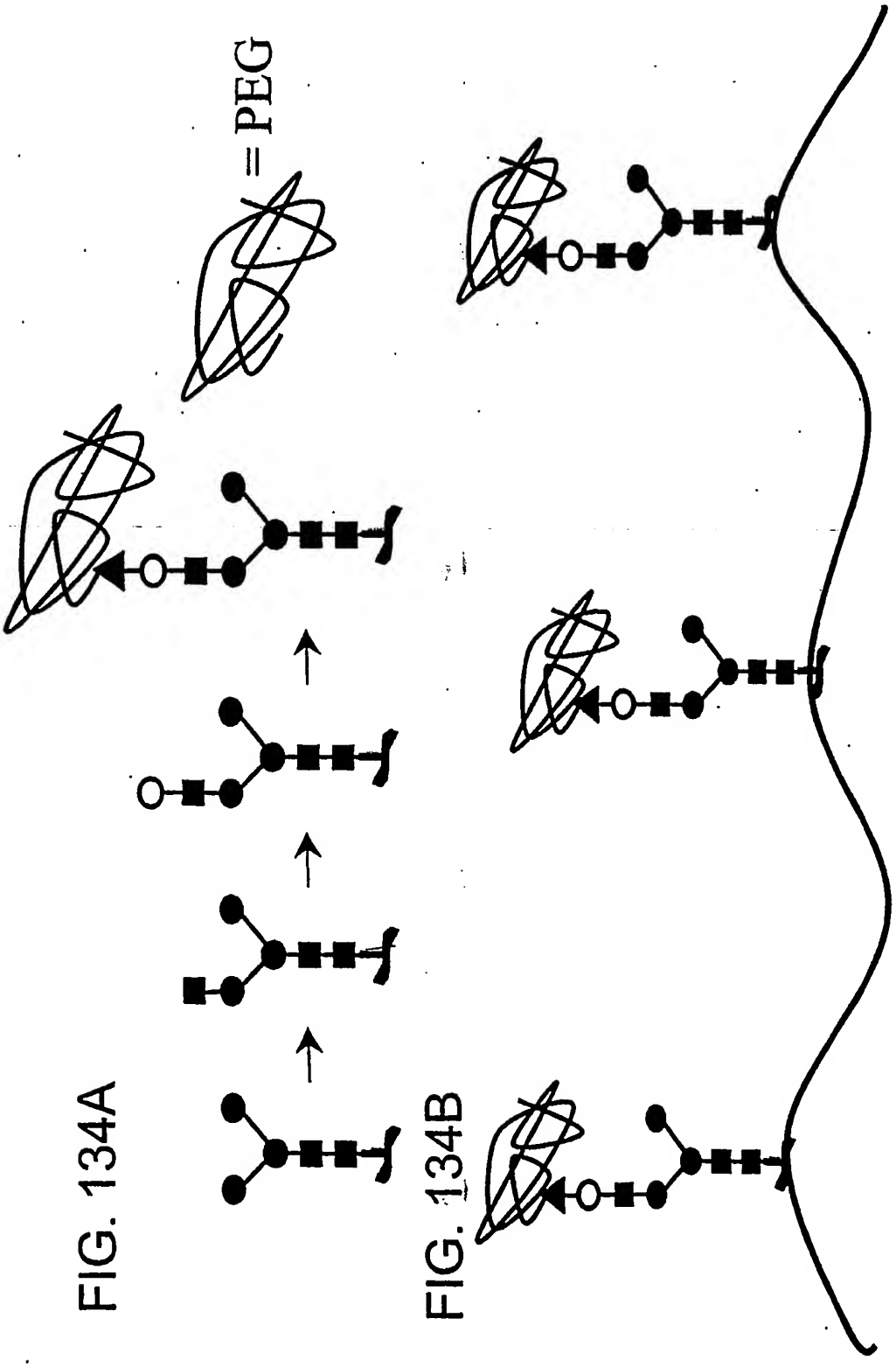

FIG. 134A

FIG. 134B

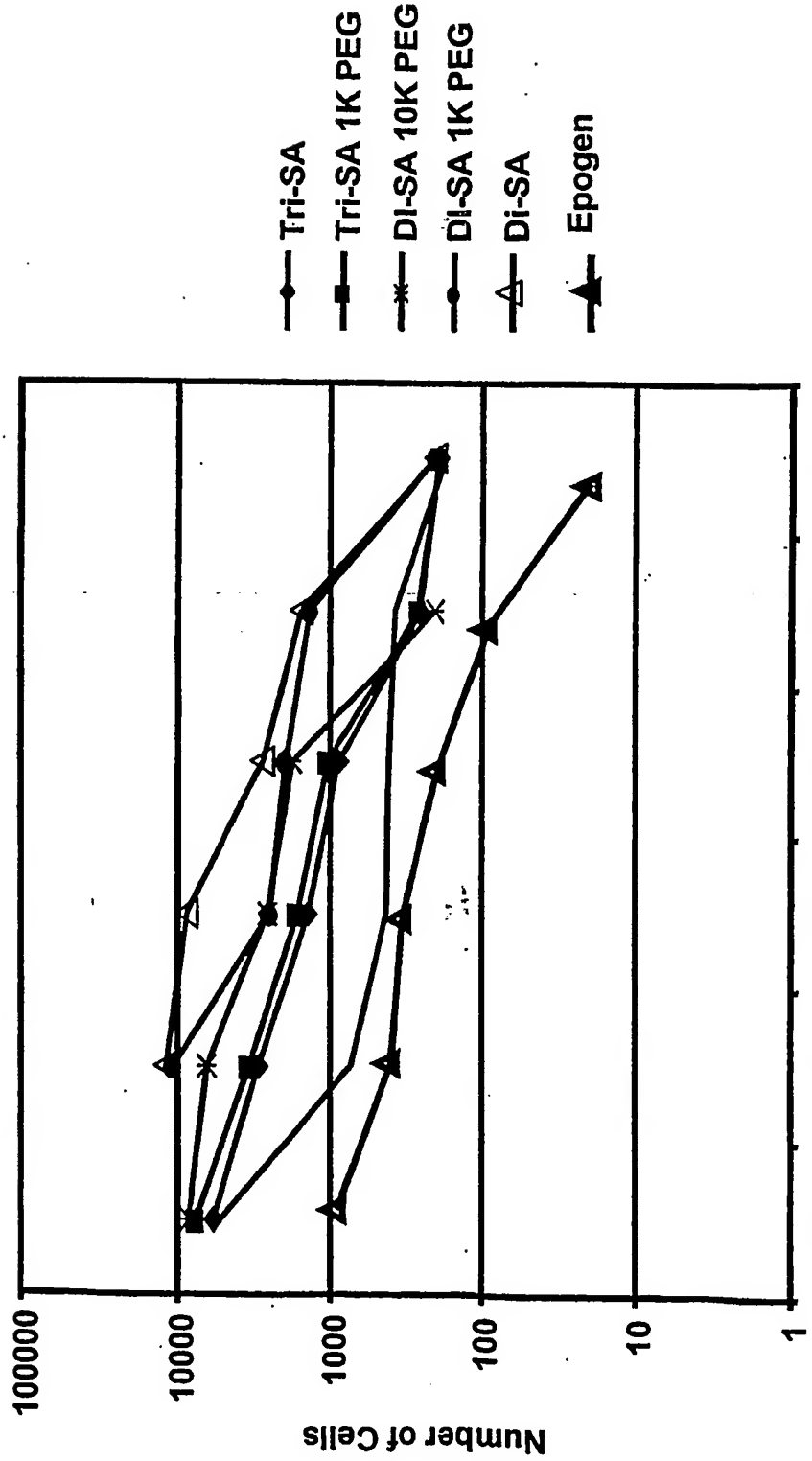
Tri-SA
Tri-SA 1K PEG
DI-SA 10K PEG
Di-SA 1K PEG
Di-SA
Epogen
Number of Cells
100000
10000
1000
100
10
1
ug/mL EPO
10
5
2
1
0.5
0

FIG. 135

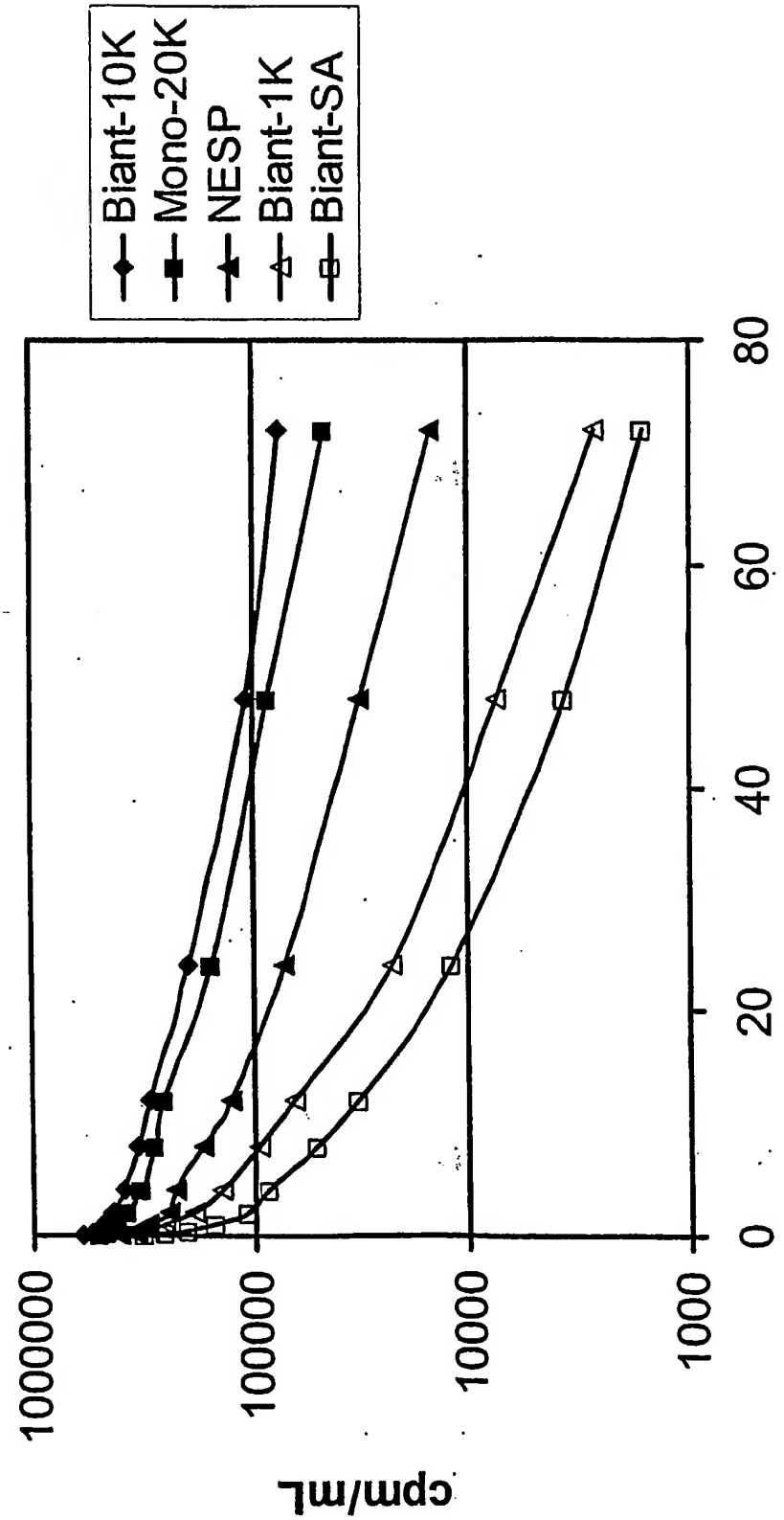
Biant-10K
Mono-20K
NESP
Biant-1K
Biant-SA
1000000
100000
10000
1000
cpm/mL
0
20
40
60
80
Time (hours)

FIG. 136

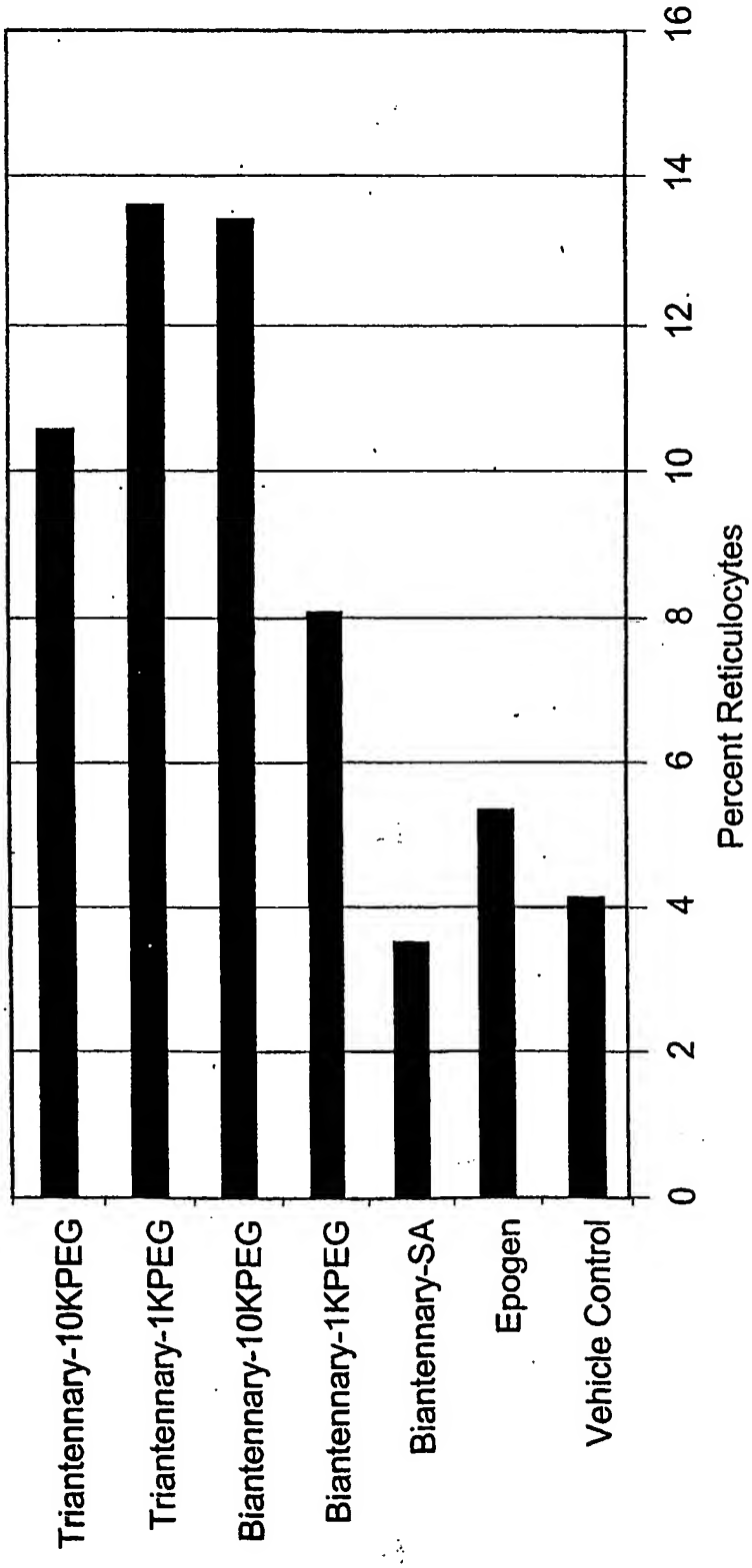
Triantennary-10KPEG
Triantennary-1KPEG
Biantennary-10KPEG
Biantennary-1KPEG
Biantennary-SA
Epogen
Vehicle Control
0
2
4
6
8
10
12
14
16
Percent Reticulocytes

FIG. 137

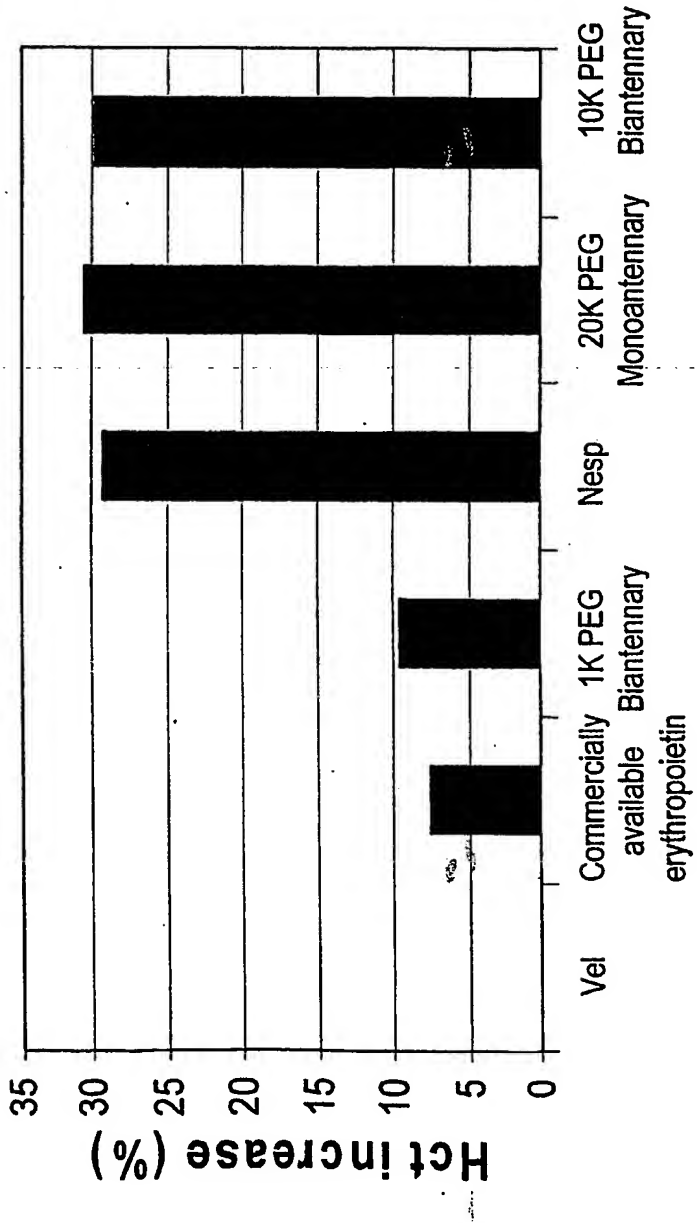
Hct increase (%)
0
5
10
15
20
25
30
35
Vel
Commercially available erythropoietin
1K PEG Biantennary
Nesp
20K PEG Monoantennary
10K PEG Biantennary

FIG. 138

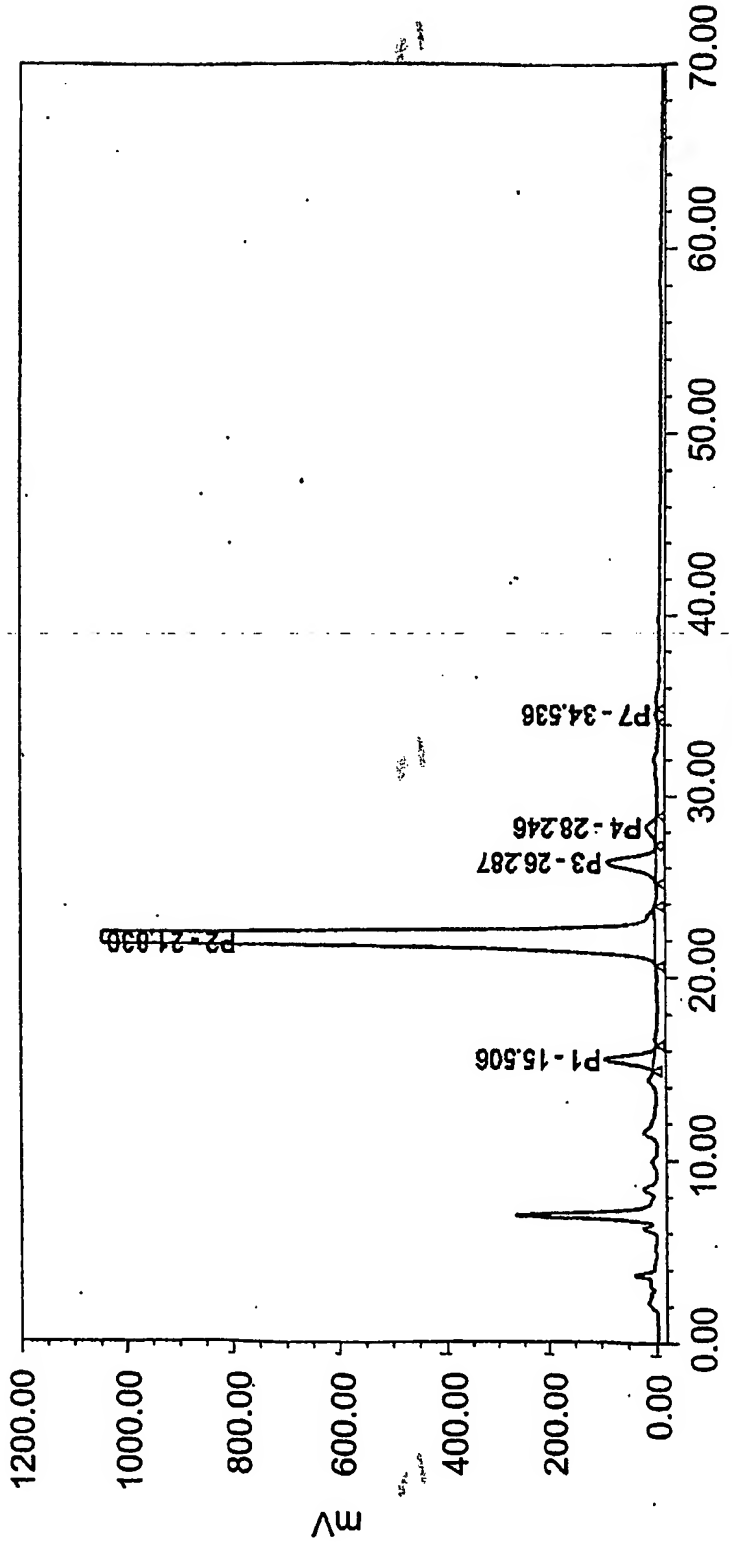
mV
1200.00
1000.00
800.00
600.00
400.00
200.00
0.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
Minutes
P1 - 15.506
P2 - 21.830
P3 - 26.287
P4 - 28.246
P7 - 34.536

FIG. 139A

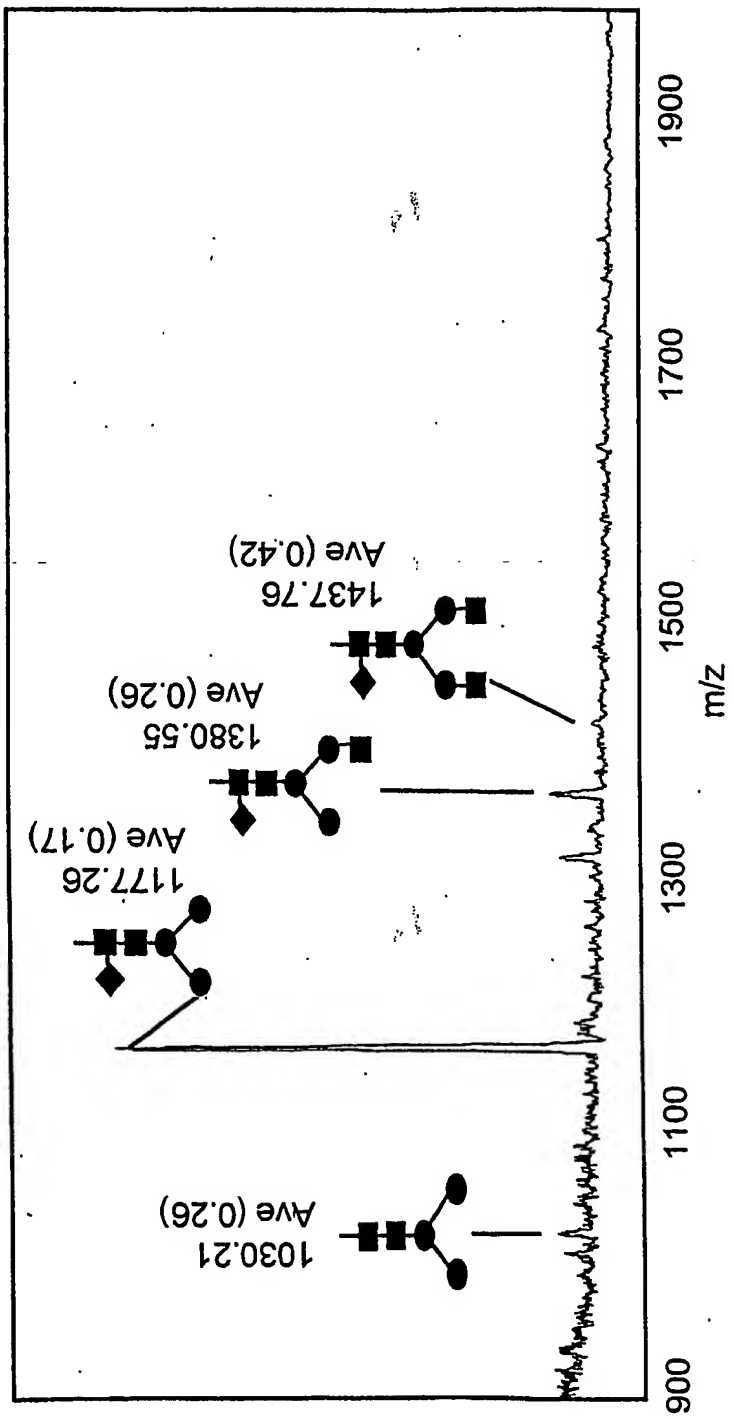
1030.21
Ave (0.26)
1177.26
Ave (0.17)
1380.55
Ave (0.26)
1437.76
Ave (0.42)
900
1100
1300
1500
1700
1900
m/z

FIG. 139B

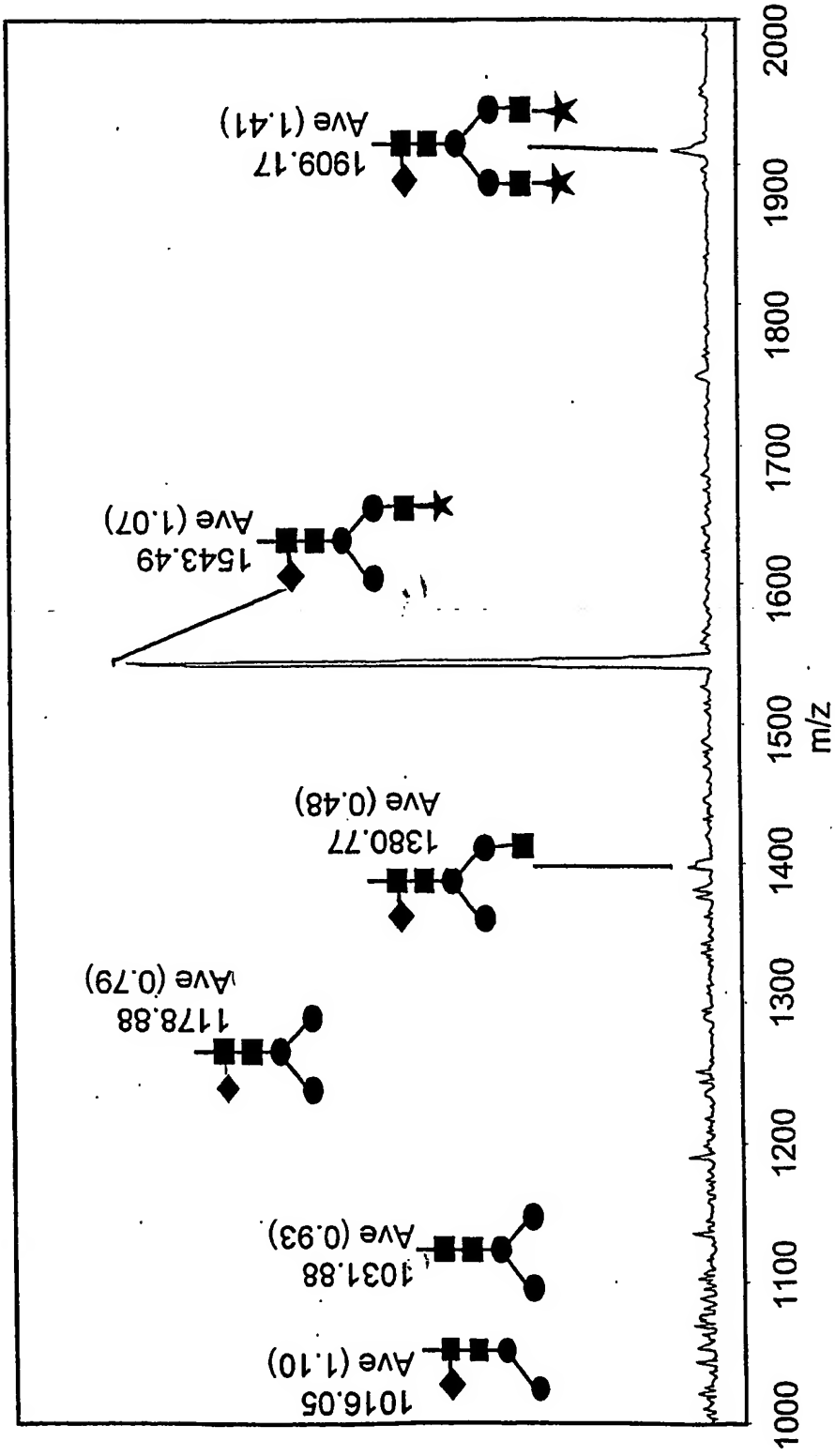
1016.05
Ave (1.10)
1031.88
Ave (0.93)
1178.88
Ave (0.79)
1380.77
Ave (0.48)
1543.49
Ave (1.07)
1909.17
Ave (1.41)
1000
1100
1200
1300
1400
1500
1600
1700
1800
1900
2000
m/z

FIG. 140

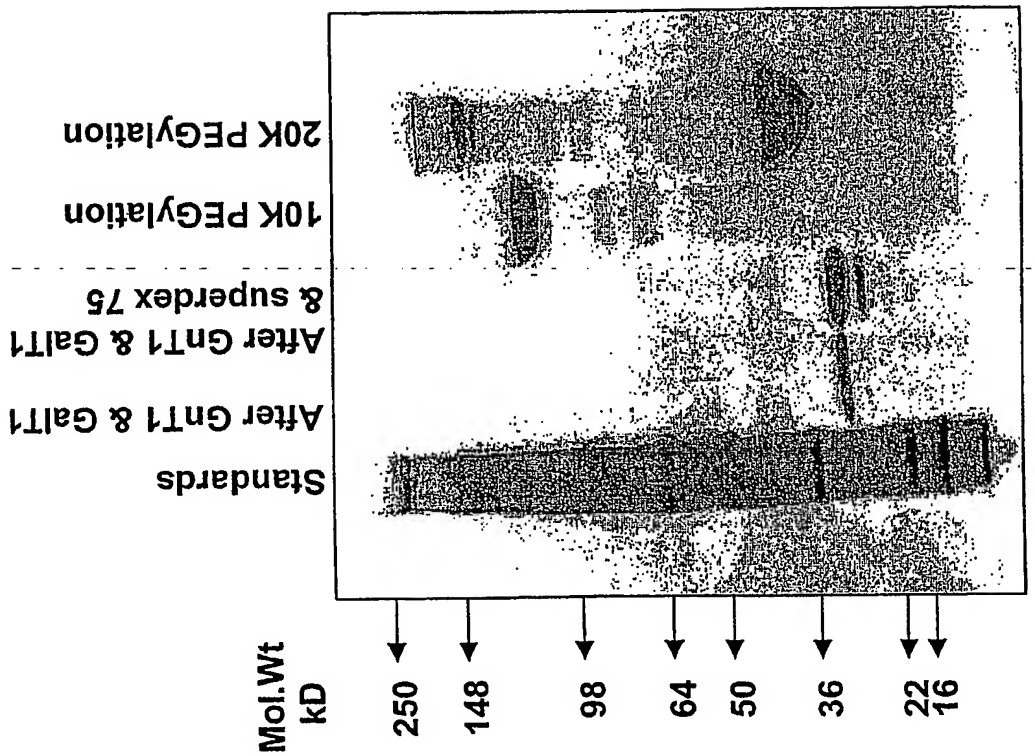
Standards
After GnT1 & GalT1
After GnT1 & GalT1 & superdex 75
10K PEGylation
20K PEGylation
Mol.Wt kD
250
148
98
64
50
36
22
16

FIG. 141

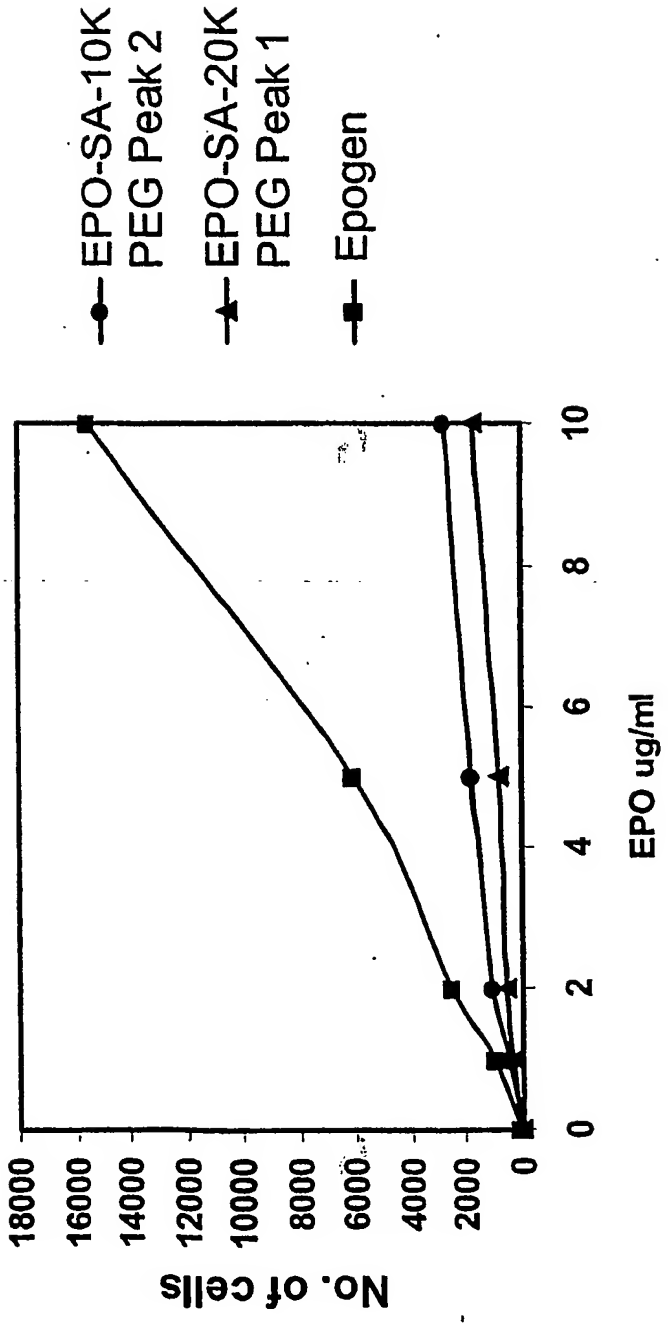
EPO-SA-10K PEG Peak 2
EPO-SA-20K PEG Peak 1
Epogen
No. of cells
18000
16000
14000
12000
10000
8000
6000
4000
2000
0
0
2
4
6
8
10
EPO ug/ml

FIG. 142

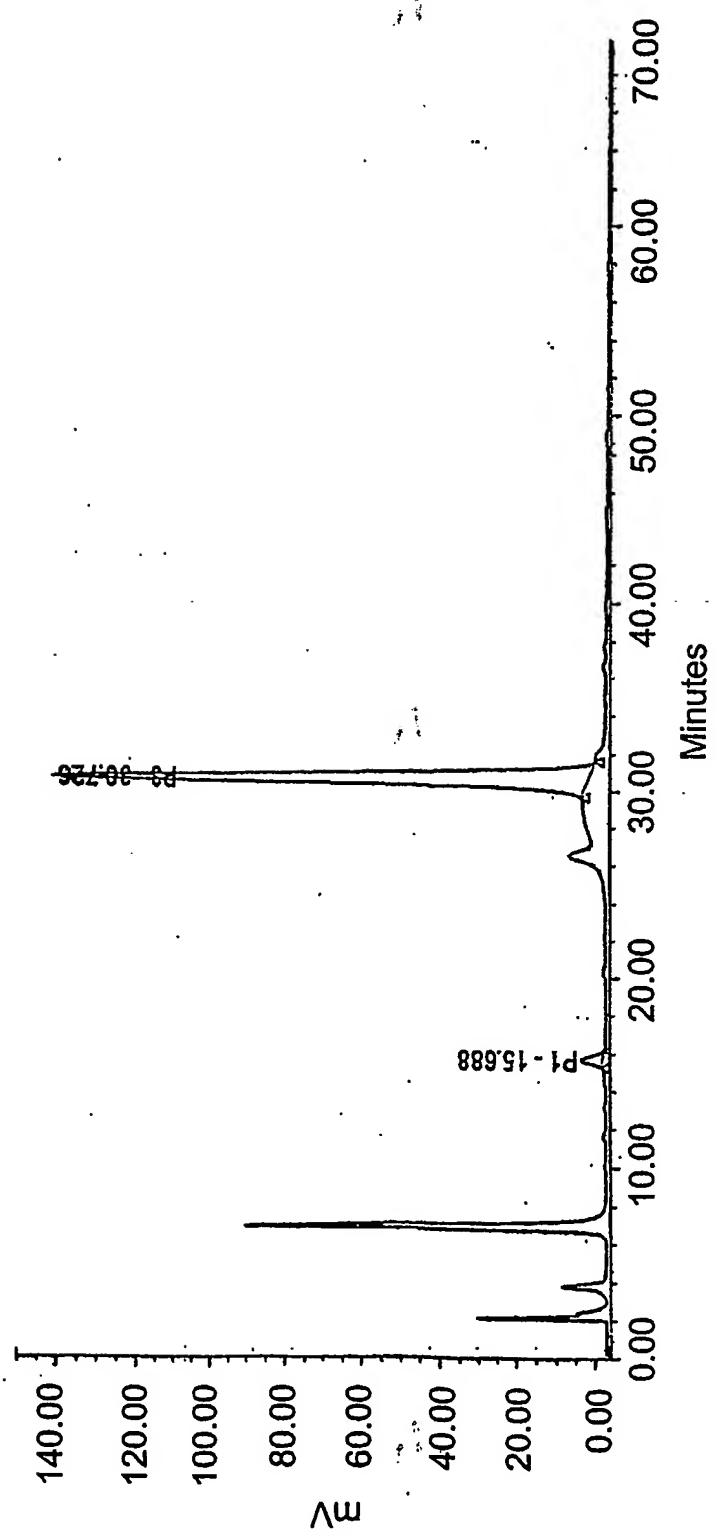
mV
140.00
120.00
100.00
80.00
60.00
40.00
20.00
0.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
Minutes
P1 - 15.688
P2 - 30.726

FIG. 143A

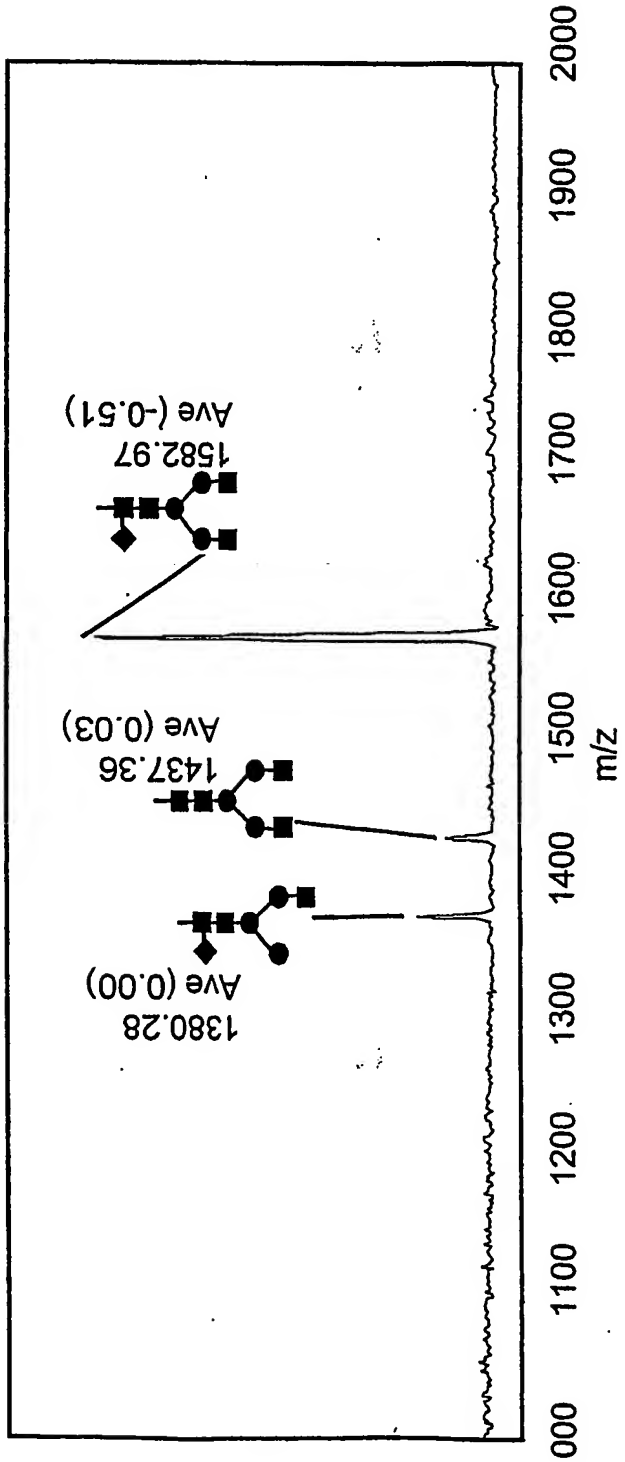
1380.28
Ave (0.00)
1437.36
Ave (0.03)
1582.97
Ave (-0.51)
1000
1100
1200
1300
1400
1500
1600
1700
1800
1900
2000
m/z

FIG. 143B

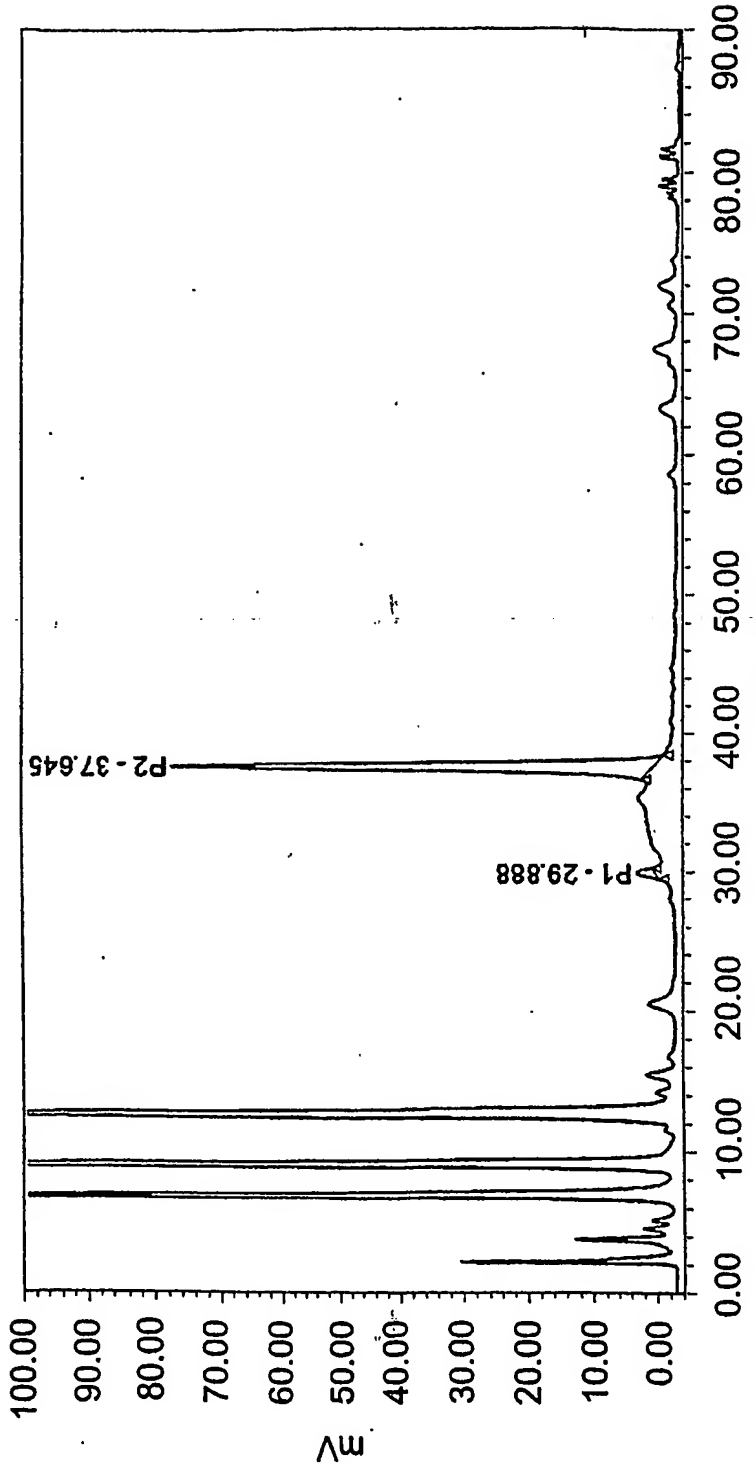
mV
100.00
90.00
80.00
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
Minutes
P1 - 29.888
P2 - 37.645

FIG. 144A

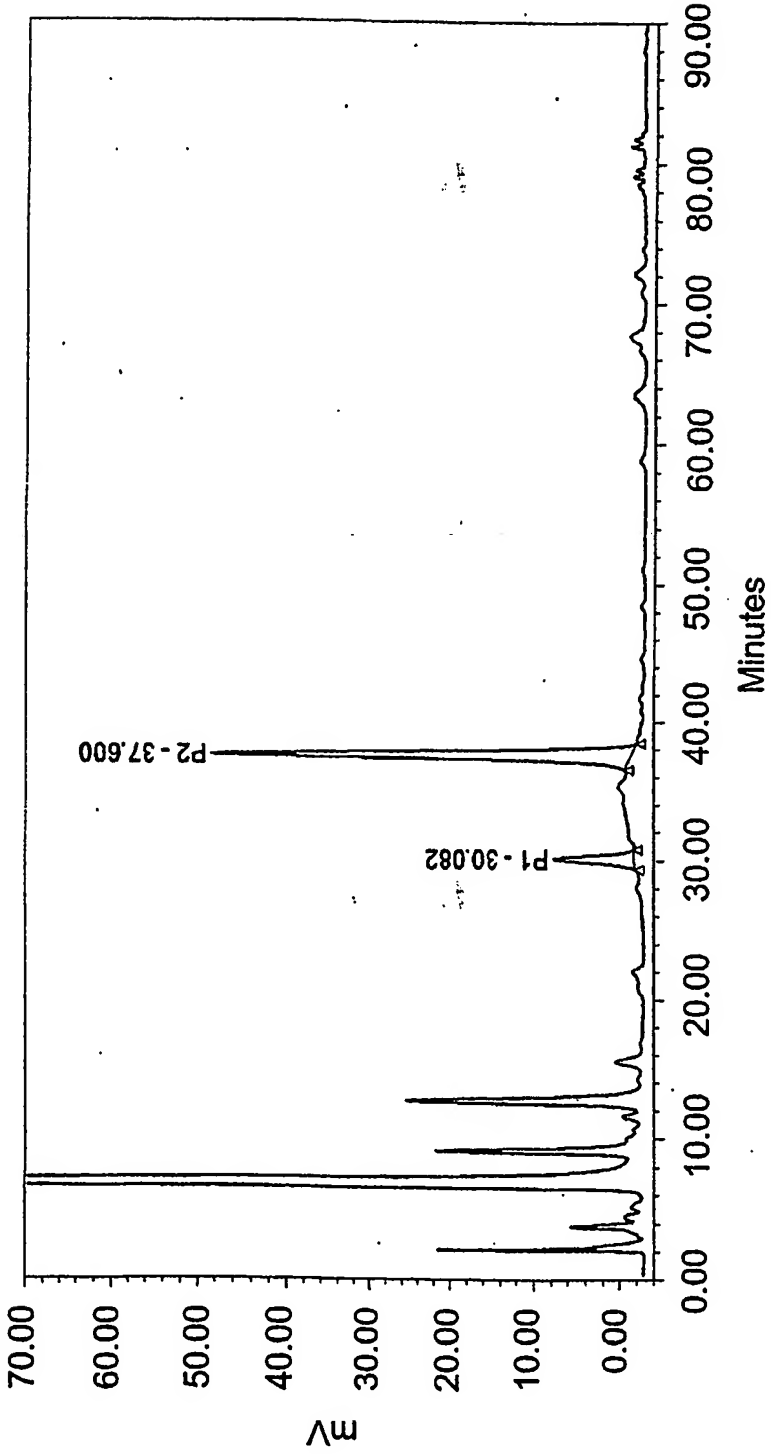
mV
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
Minutes
P1 - 30.082
P2 - 37.600

FIG. 144B

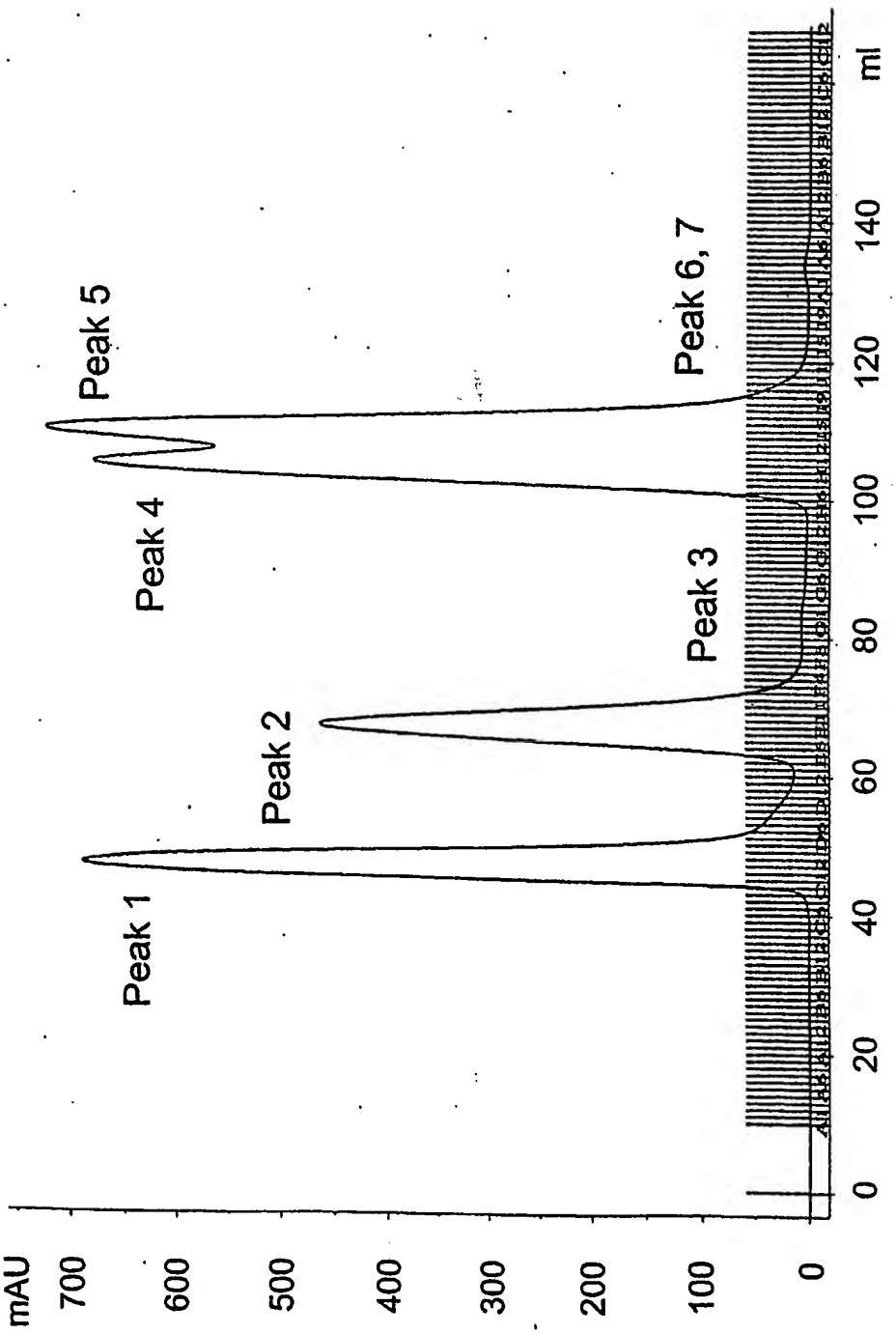
mAU
700
600
500
400
300
200
100
0
0
20
40
60
80
100
120
140
ml
Peak 1
Peak 2
Peak 3
Peak 4
Peak 5
Peak 6, 7

FIG. 145

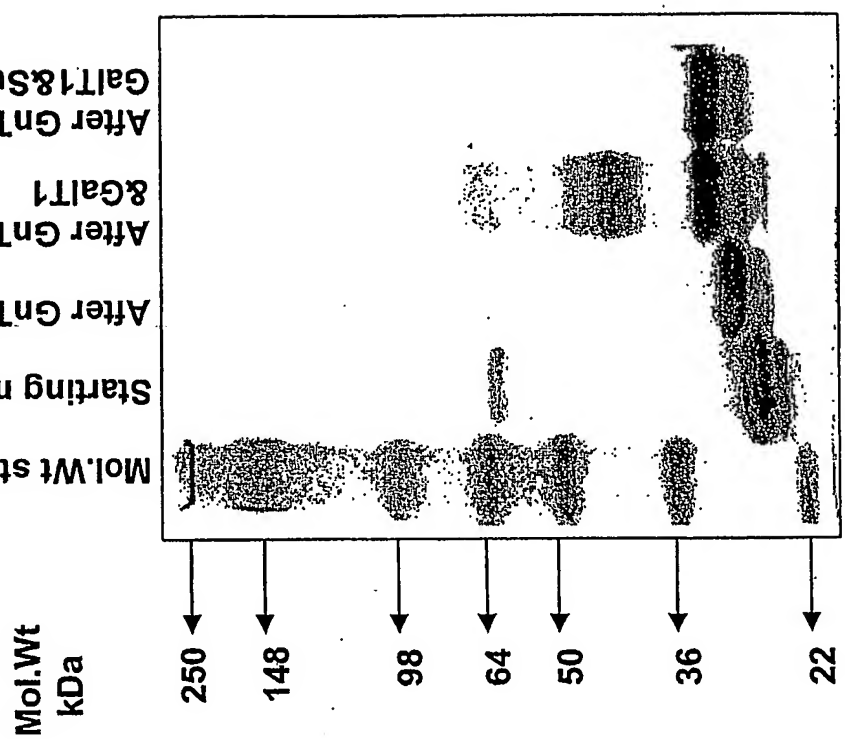
Mol.Wt standards
Starting material
After GnT1&GnT2
After GnT1,GnT2 &GalT1
After GnT1,GnT2, GalT1&Super75
Mol.Wt kDa
250
148
98
64
50
36
22

FIG. 146

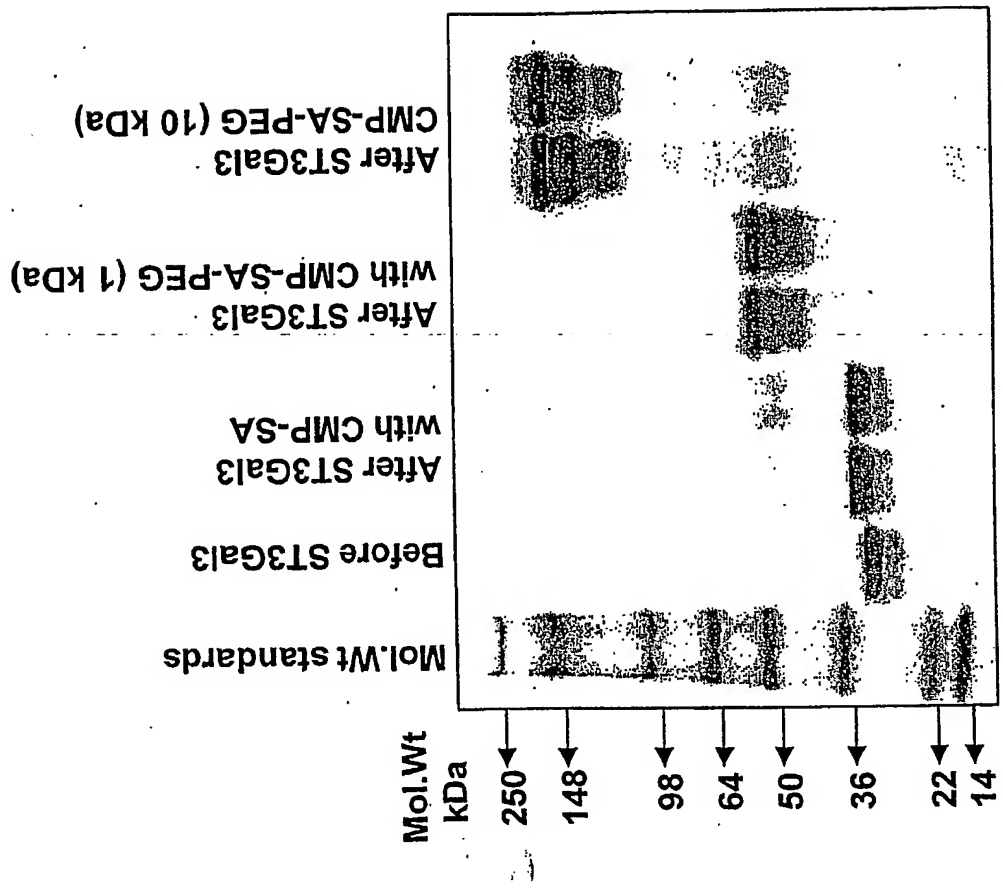
Mol.Wt standards
Before ST3Gal3
After ST3Gal3 with CMP-SA
After ST3Gal3 with CMP-SA-PEG (1 kDa)
After ST3Gal3 CMP-SA-PEG (10 kDa)
Mol.Wt kDa
250
148
98
64
50
36
22
14

FIG. 147

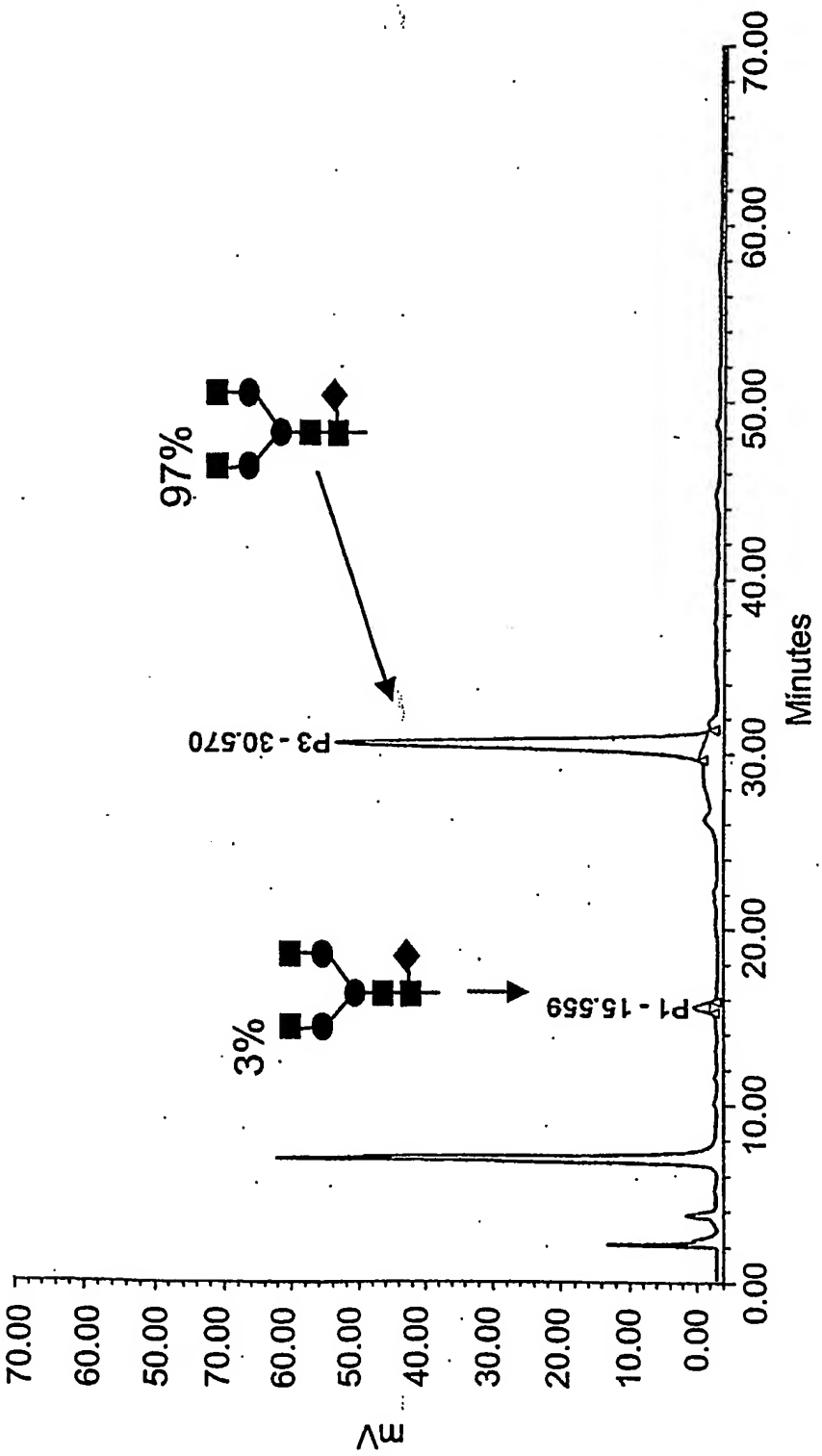
mV
70.00
60.00
50.00
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
Minutes
P1 - 15.559
P3 - 30.570
3%
97%

FIG. 148

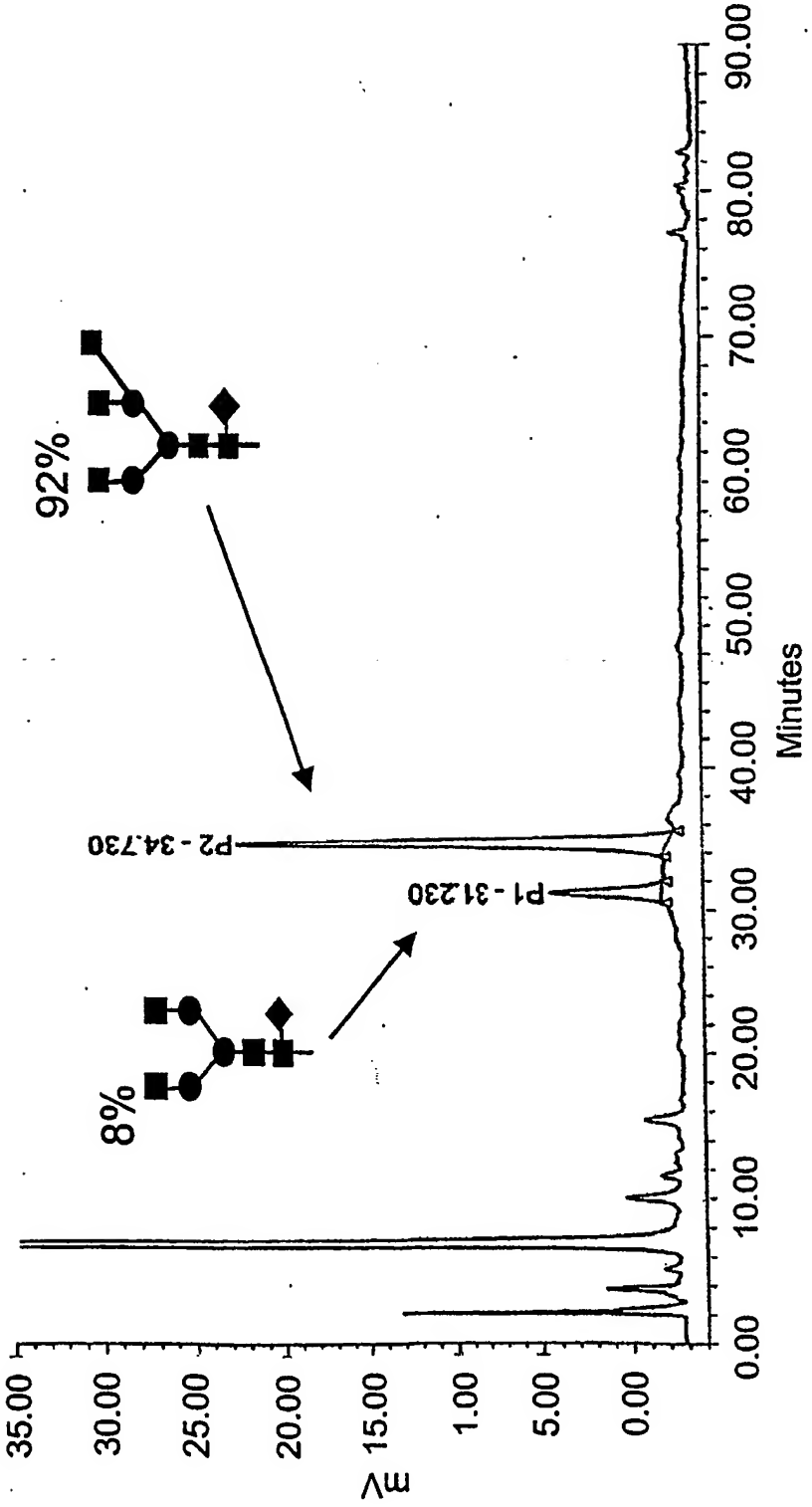
92%
8%
P2 - 34.730
P1 - 31.230
mV
35.00
30.00
25.00
20.00
15.00
1.00
5.00
0.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
Minutes

FIG. 149

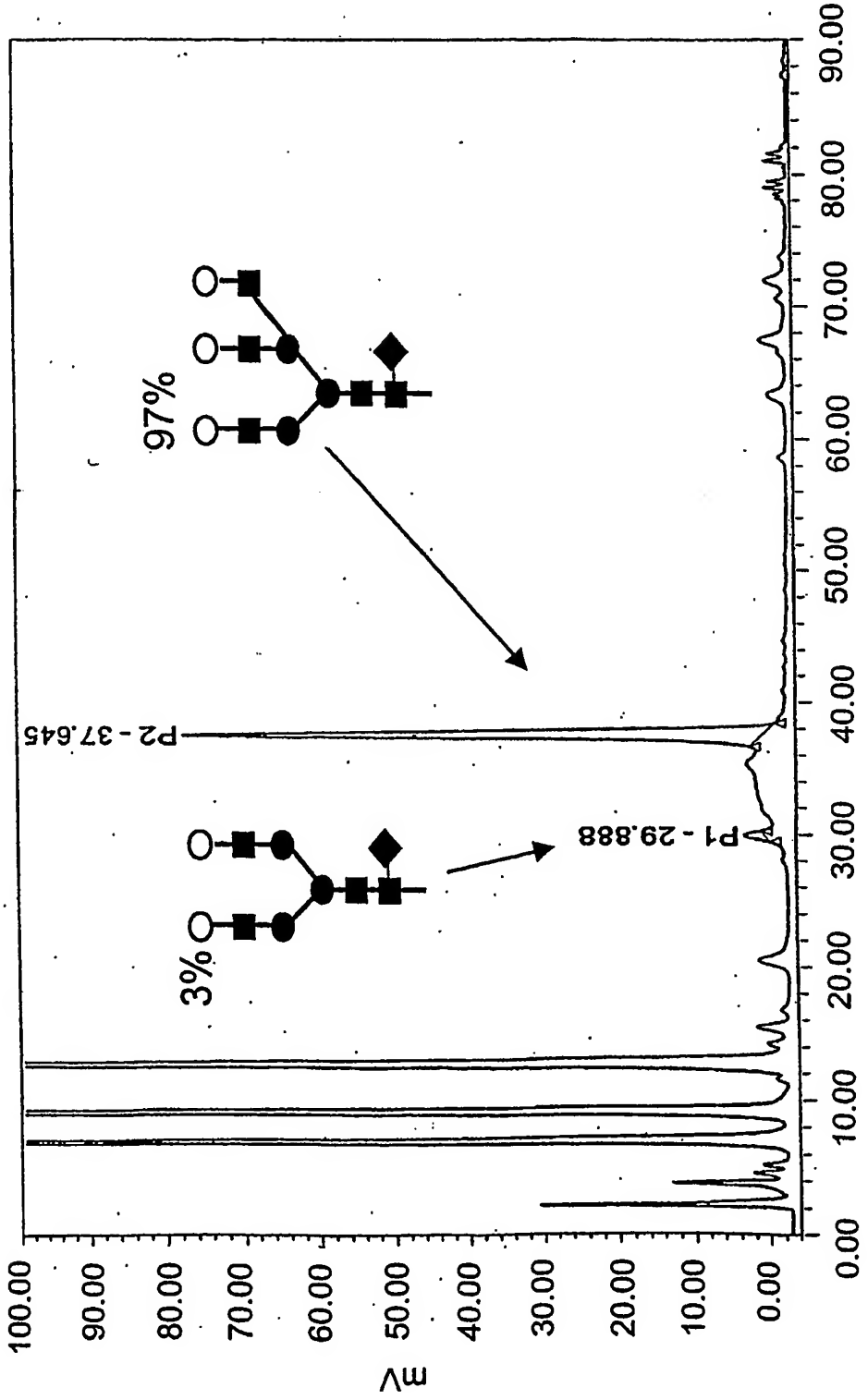
mV
100.00
90.00
80.00
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
Minutes
P1 - 29.888
P2 - 37.645
3%
97%

FIG. 150

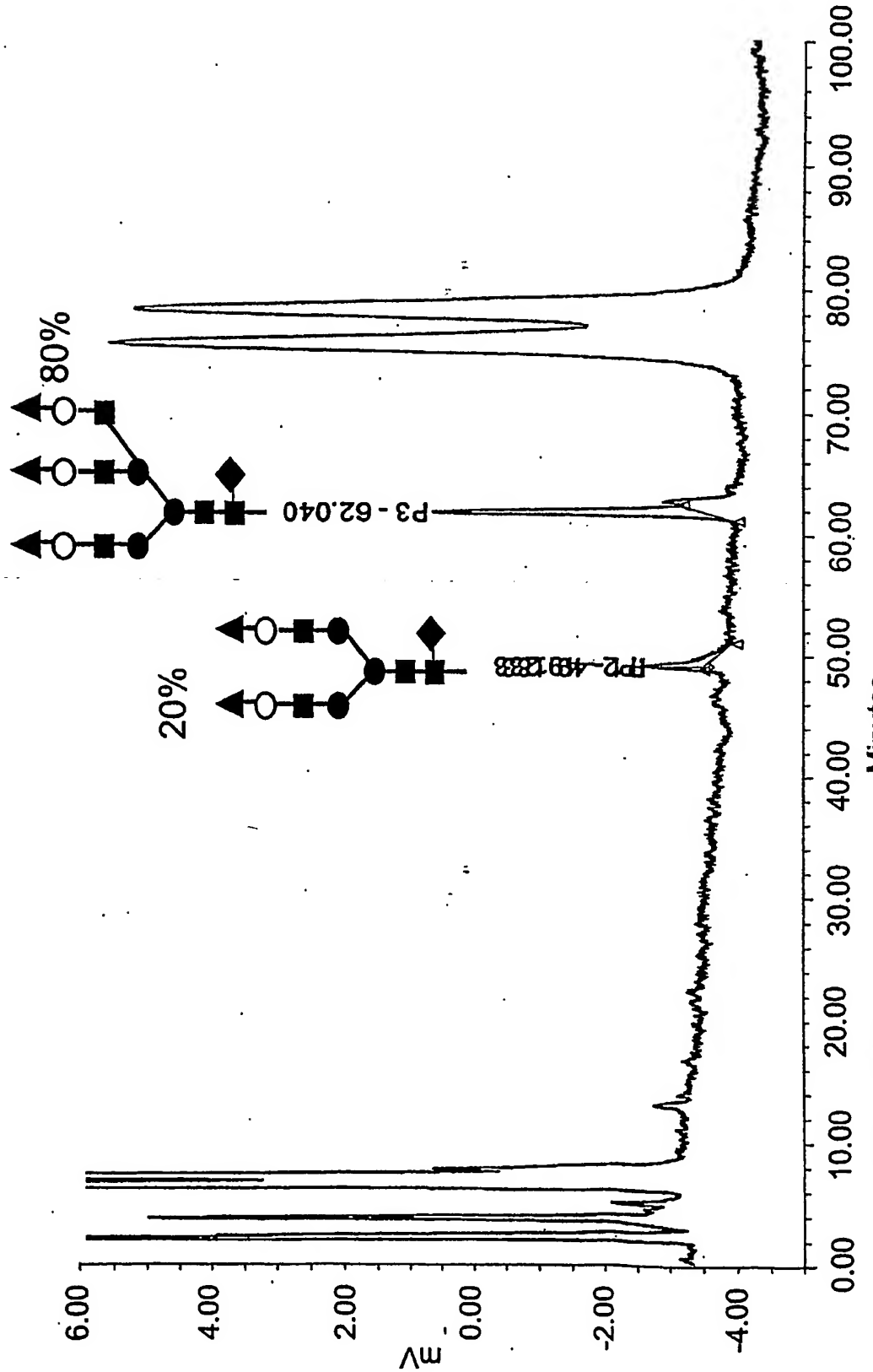
80%
20%
P3 - 62.040
mV
6.00
4.00
2.00
0.00
-2.00
-4.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
100.00
Minutes

FIG. 151

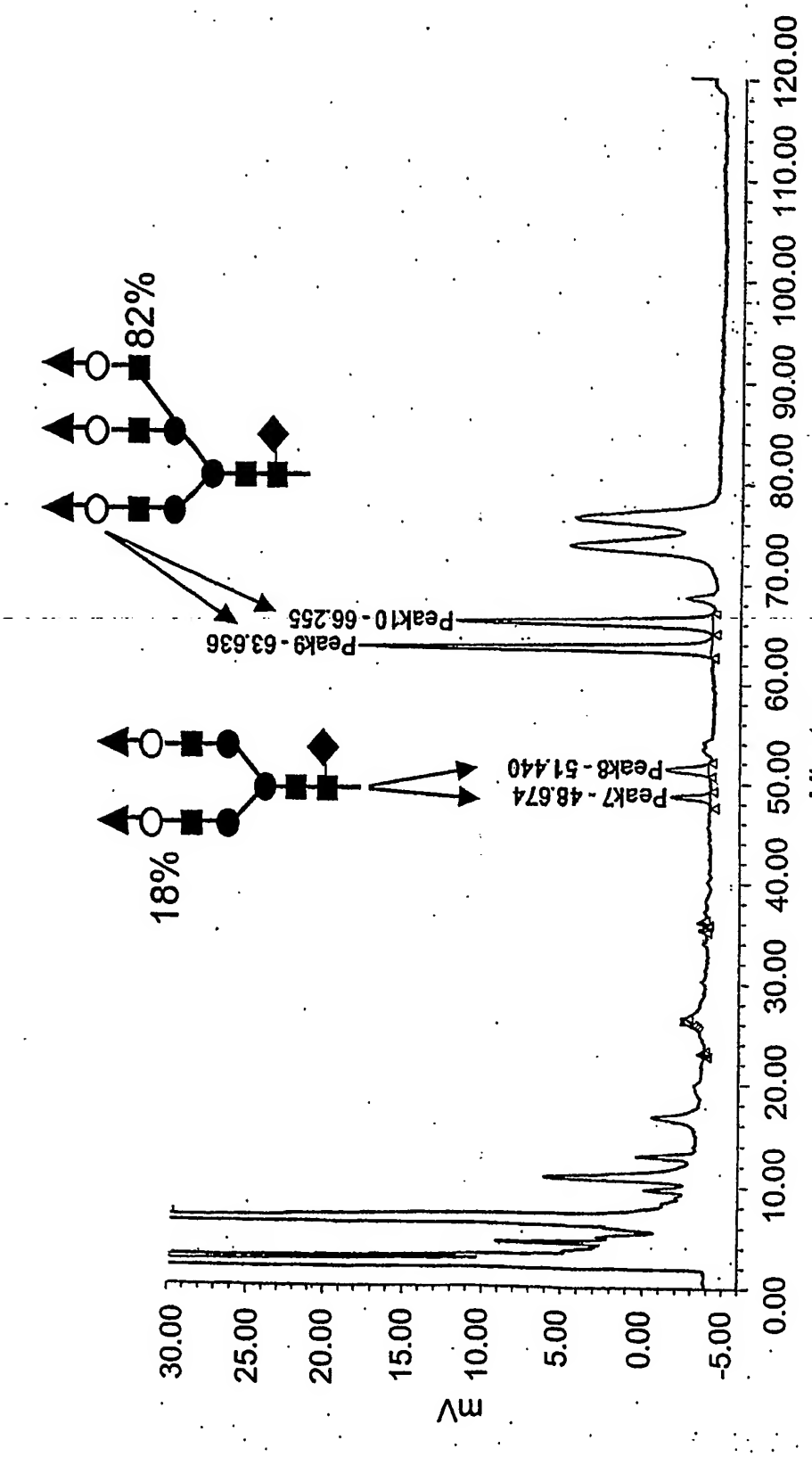
mV
30.00
25.00
20.00
15.00
10.00
5.00
0.00
-5.00
0.00
10.00
20.00
30.00
40.00
50.00
60.00
70.00
80.00
90.00
100.00
110.00
120.00
Minutes
Peak7 - 48.574
Peak8 - 51.440
Peak9 - 63.636
Peak10 - 66.255
18%
82%

FIG. 152

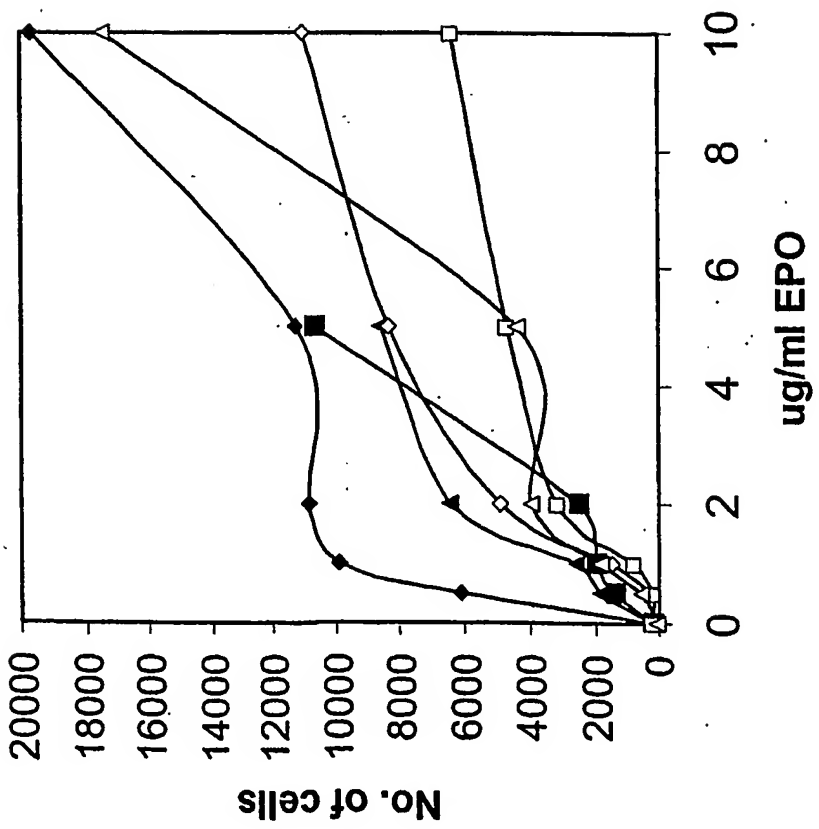
Di-SA P112
DI-SA 10K PEG P115
DI-SA 1K PEG P114
Tri-SA ST6 + ST3 P129
Tri-SA ST3 P128
Epogen
No. of cells
20000
18000
16000
14000
12000
10000
8000
6000
4000
2000
0
0
2
4
6
8
10
ug/ml EPO

FIG. 153

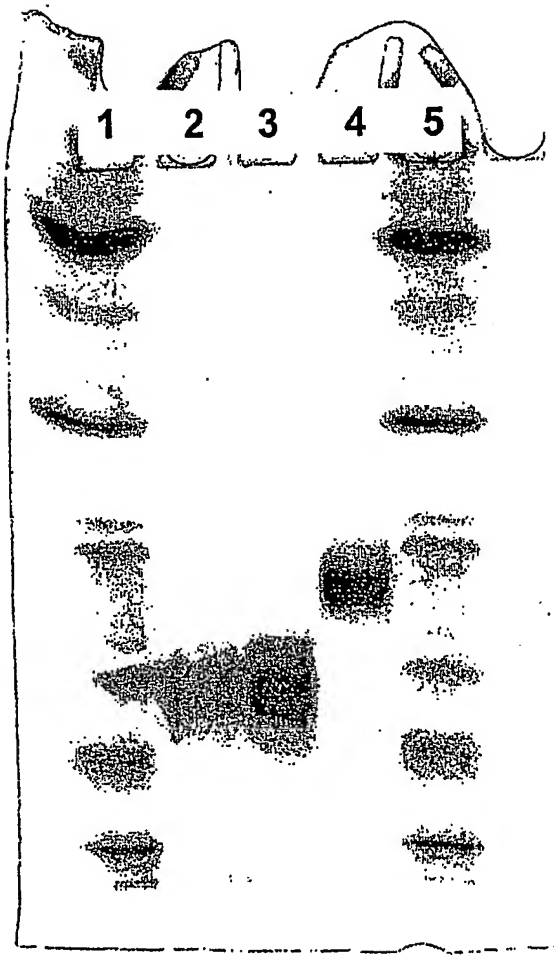

FIG. 154

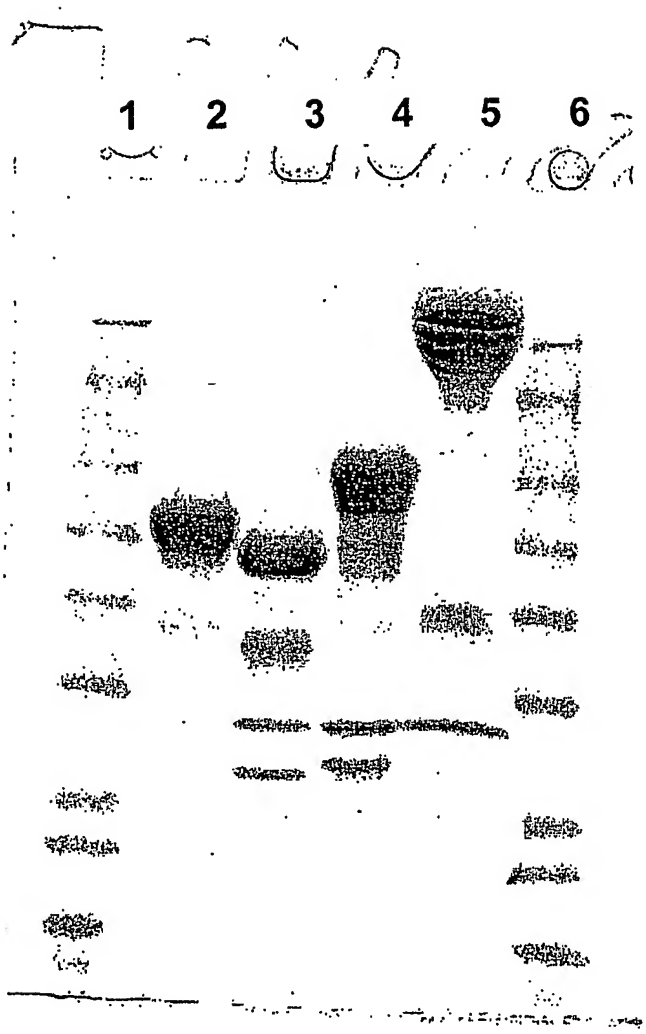

FIG. 155

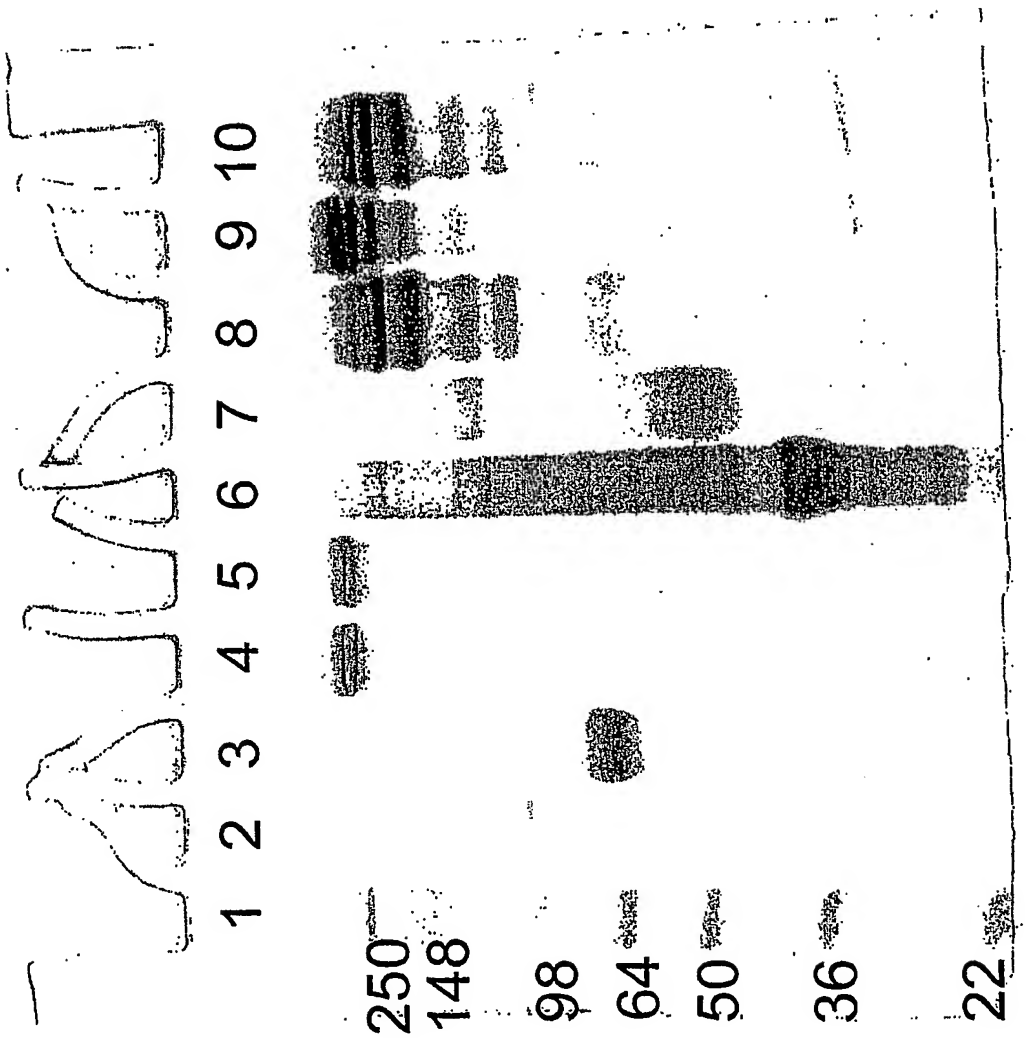

FIG. 156

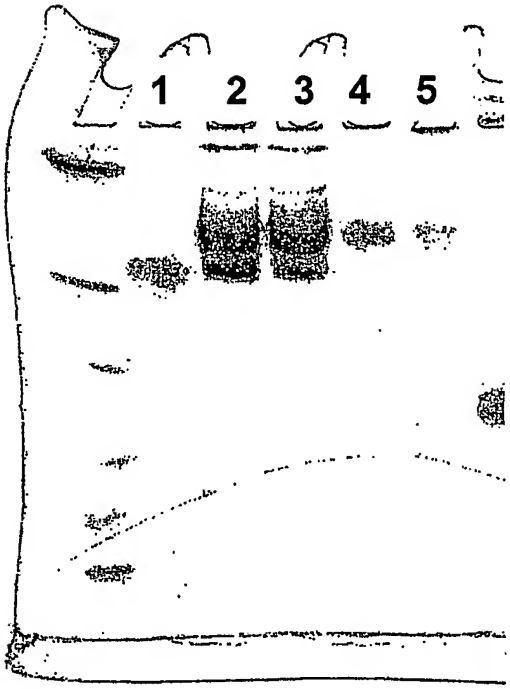

FIG. 157

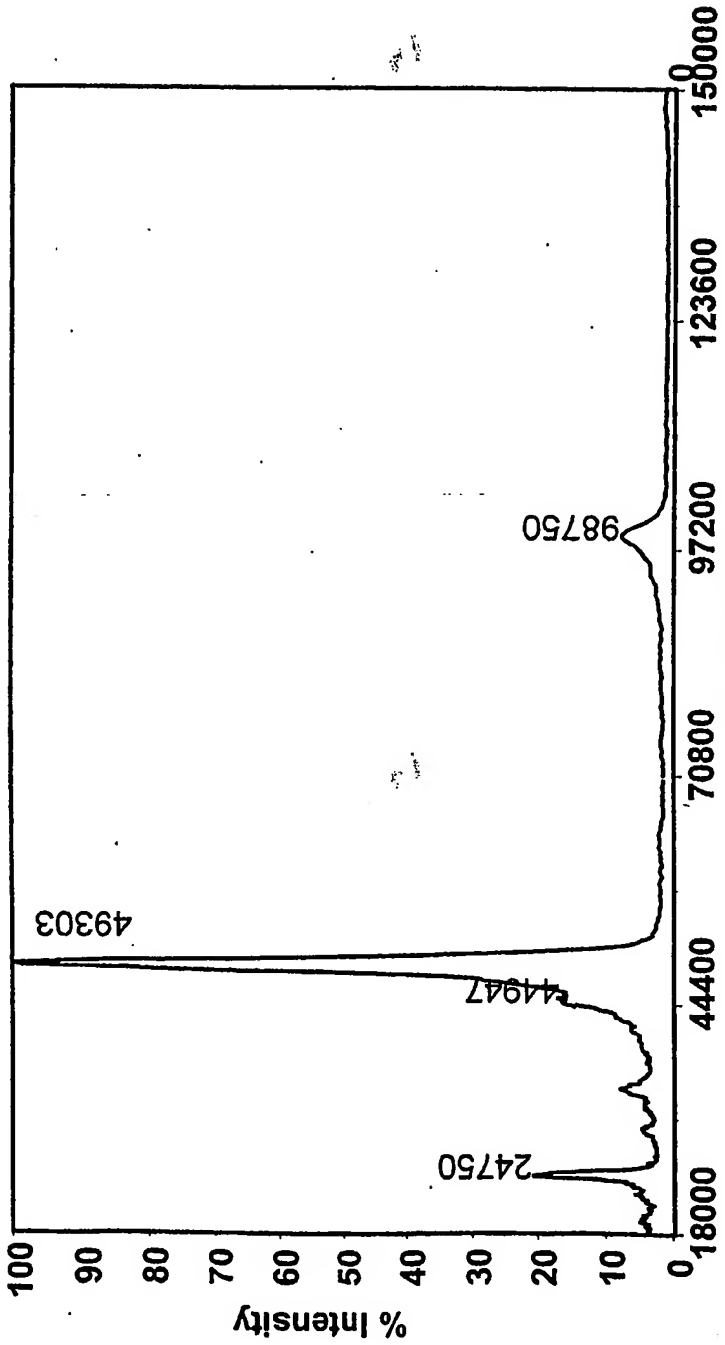
% Intensity
100
90
80
70
60
50
40
30
20
10
0
18000
44400
70800
97200
123600
150000
Mass (m/z)
24750
44947
49303
98750

FIG. 158

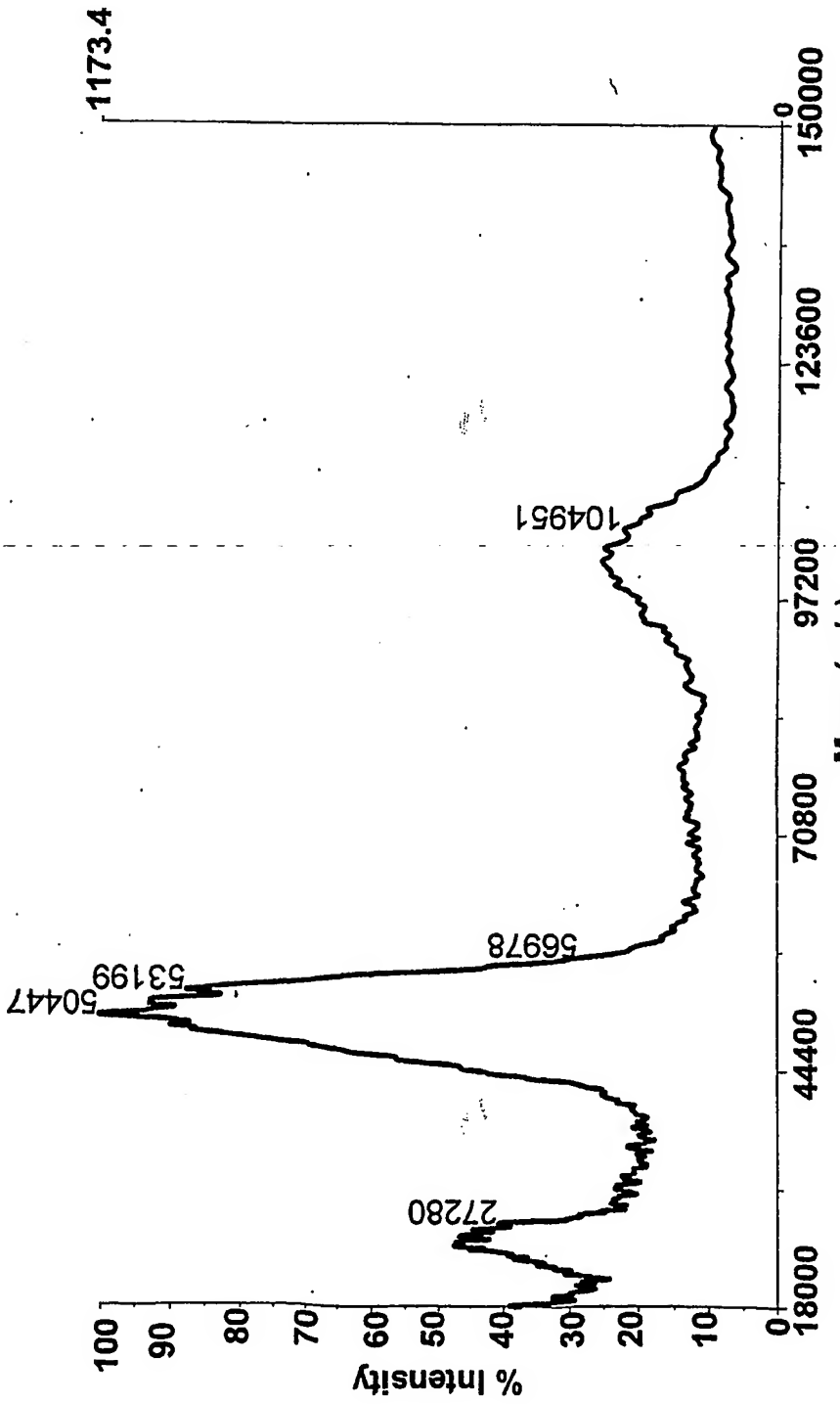
1173.4
104951
56978
53199
50447
27280
% Intensity
Mass (m/z)
0
10
20
30
40
50
60
70
80
90
100
18000
44400
70800
97200
123600
150000

FIG. 159

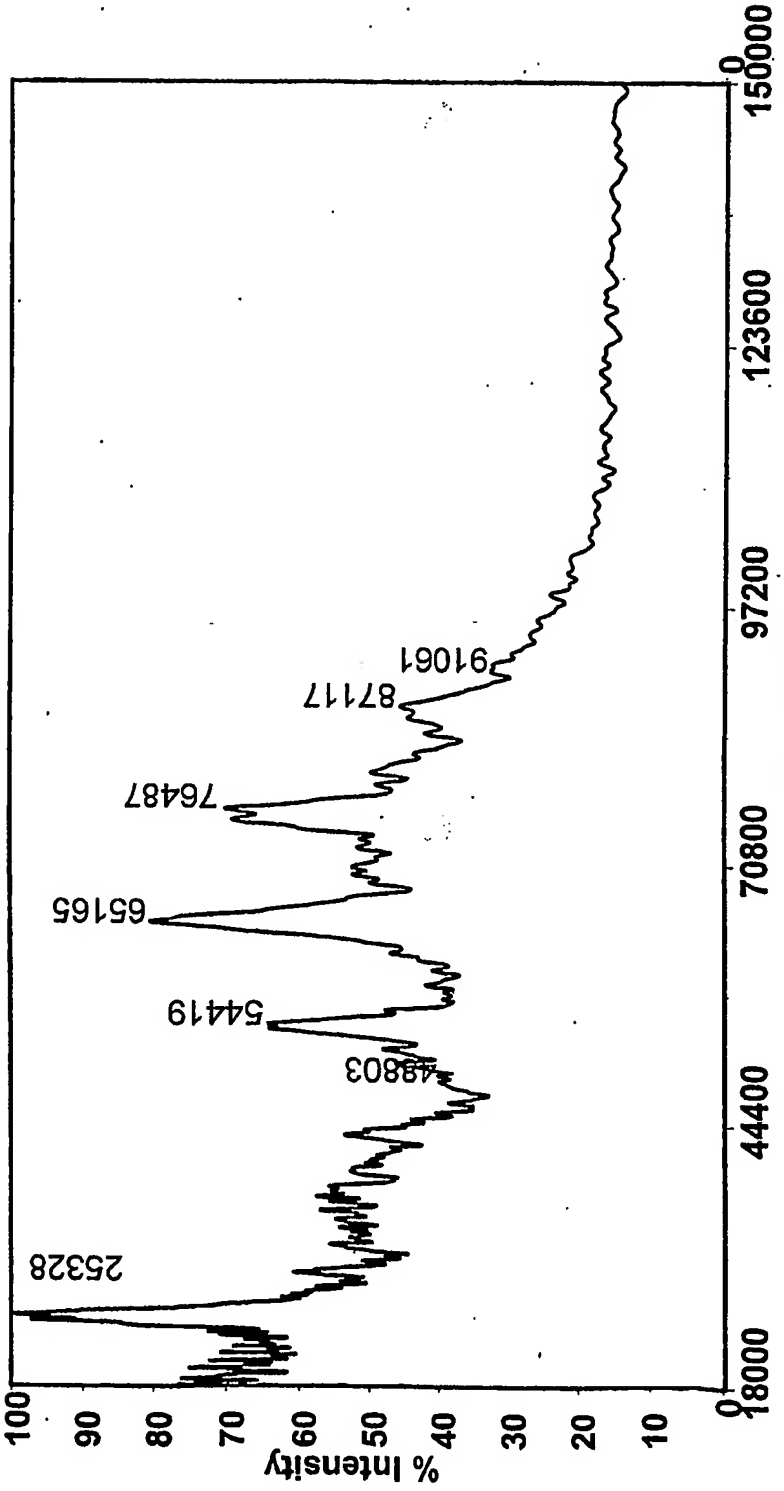
% Intensity
100
90
80
70
60
50
40
30
20
10
0
18000
44400
70800
97200
123600
150000
Mass (m/z)
25328
48803
54419
65165
76487
87117
91061

FIG. 160

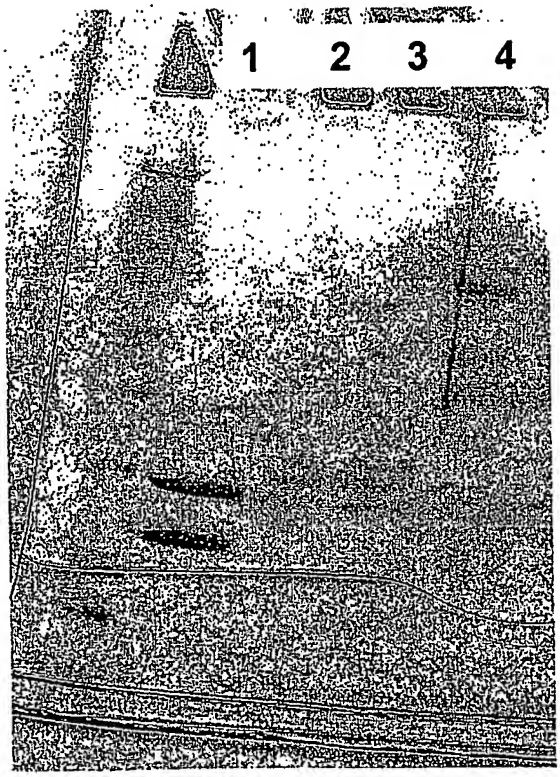

FIG. 161

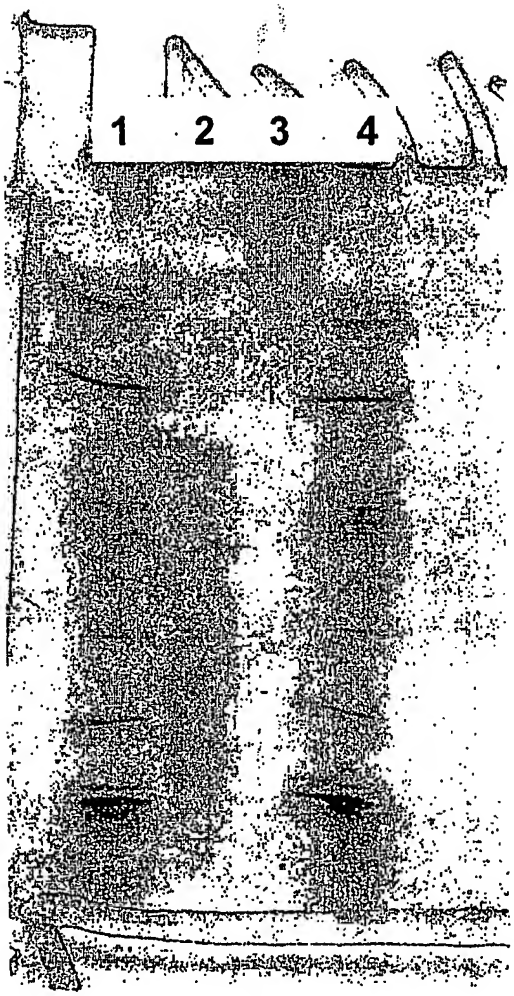

FIG. 162

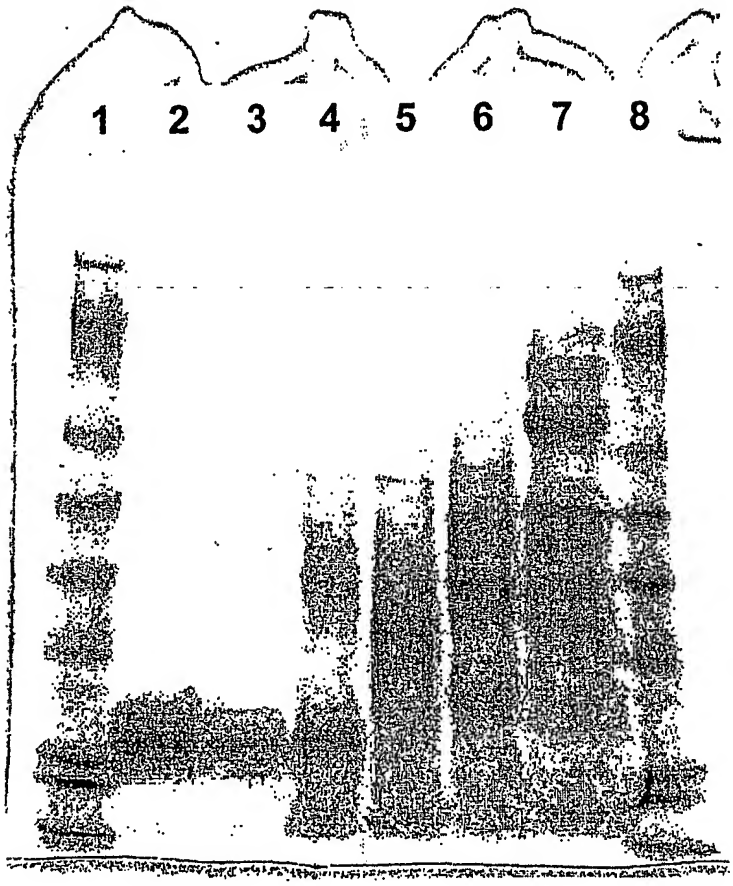

FIG. 163

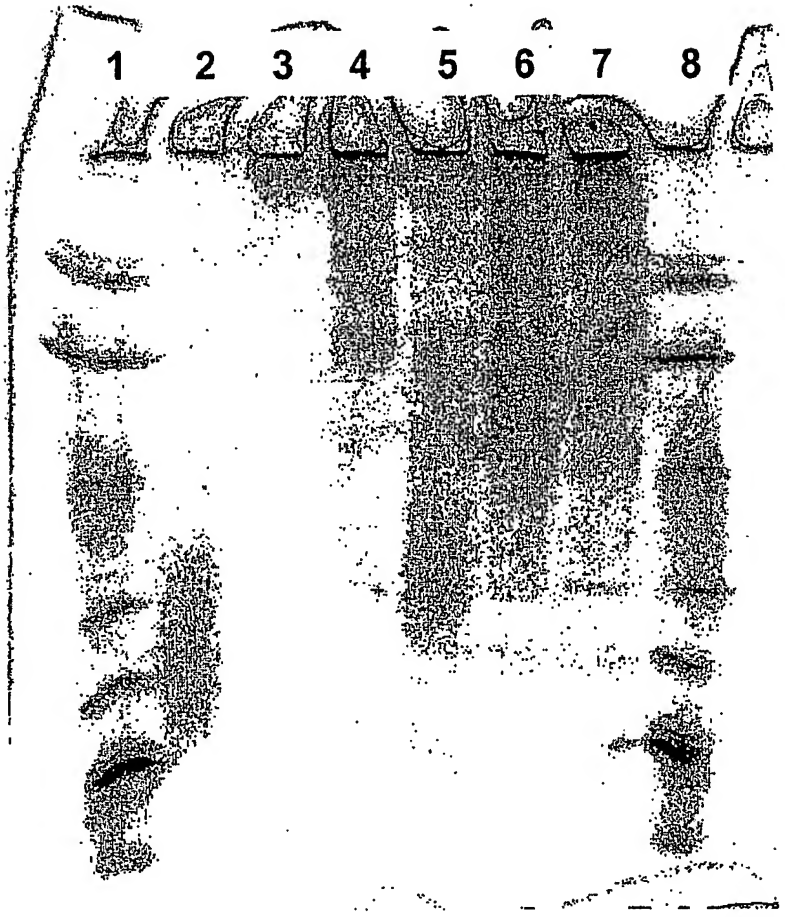

FIG. 164

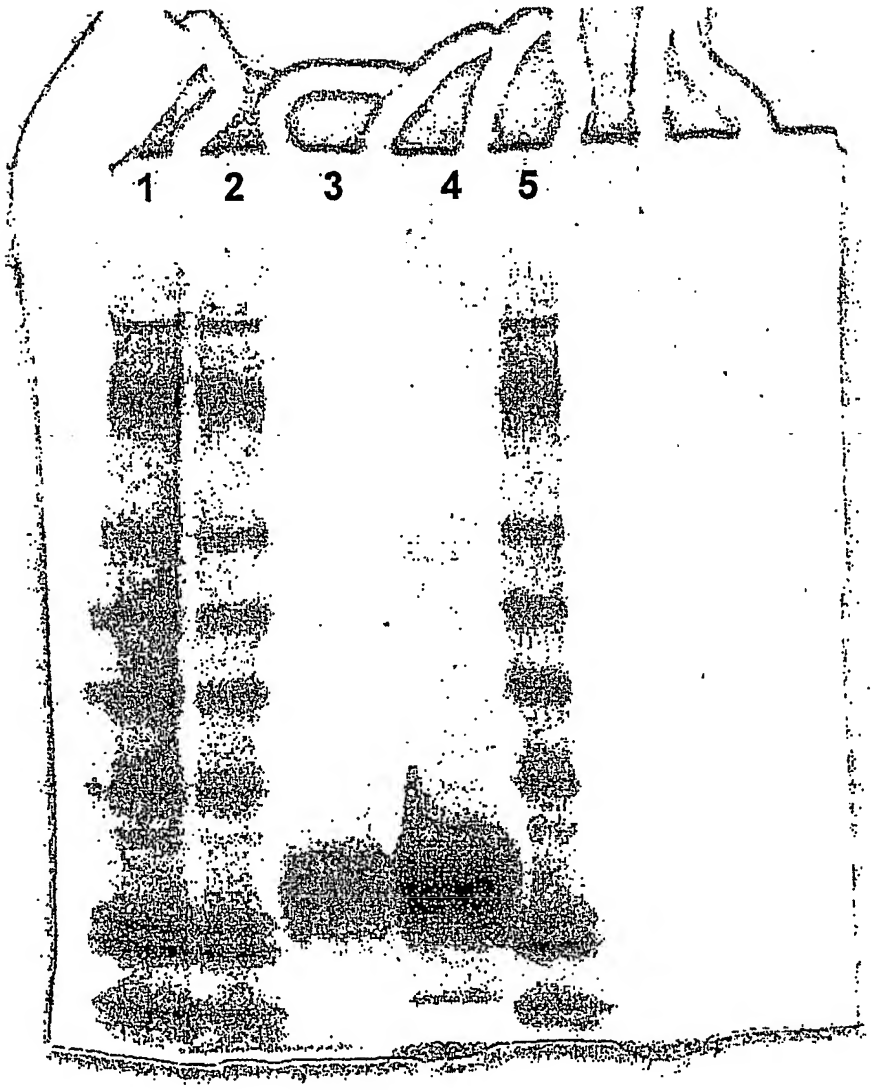

FIG. 165

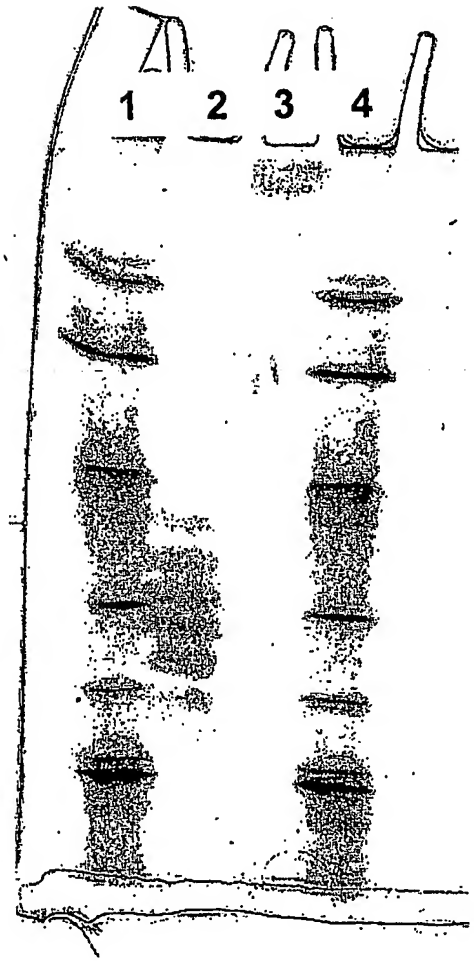

FIG. 166

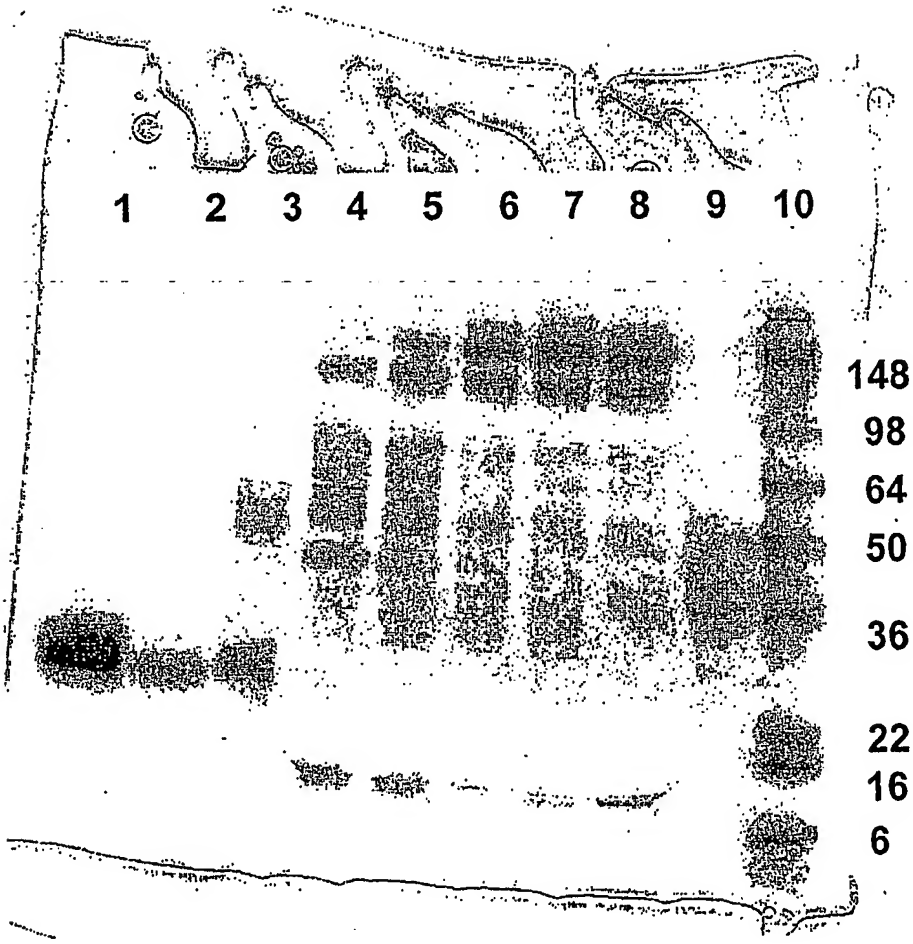

FIG. 167

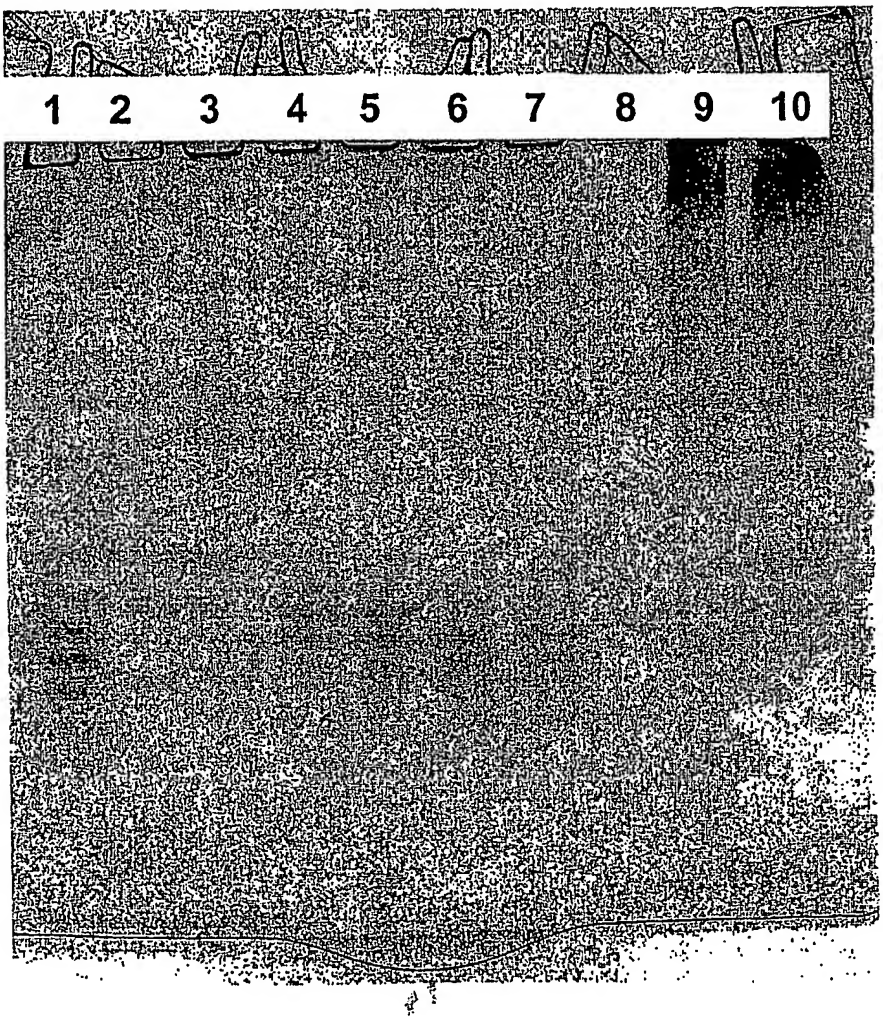

FIG. 168

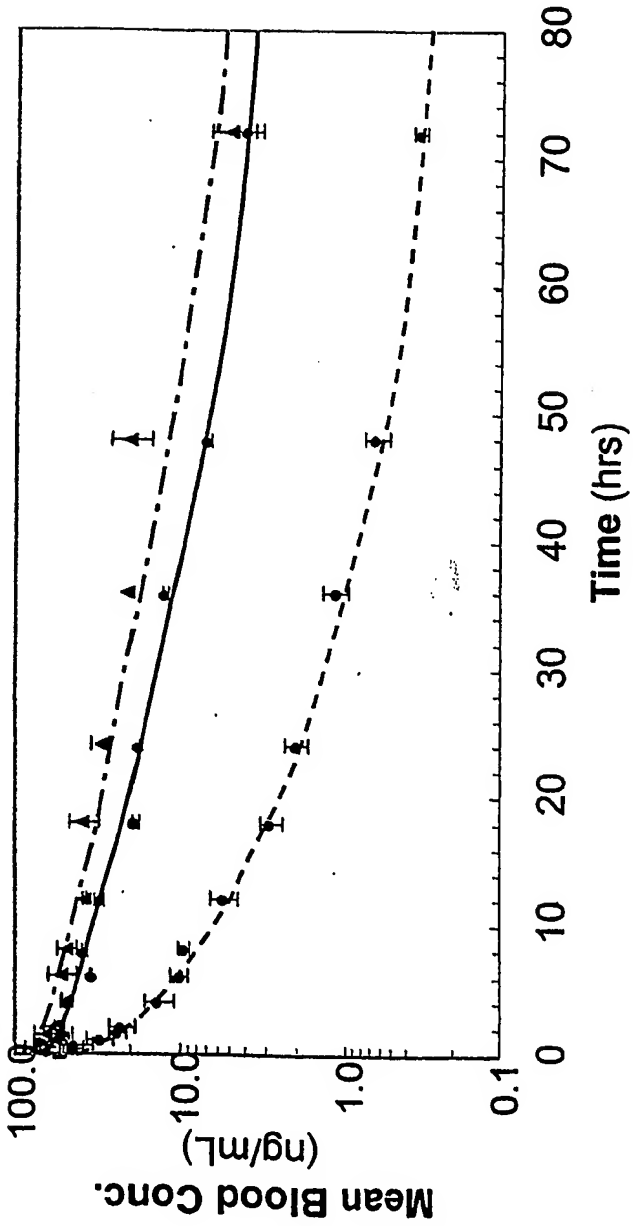
Mean Blood Conc. (ng/mL)
100.0
10.0
1.0
0.1
0
10
20
30
40
50
60
70
80
Time (hrs)
rFSH-SA-PEG (10 KDa)
rFSH-SA-PEG (1 KDa)
rFSH

FIG. 169

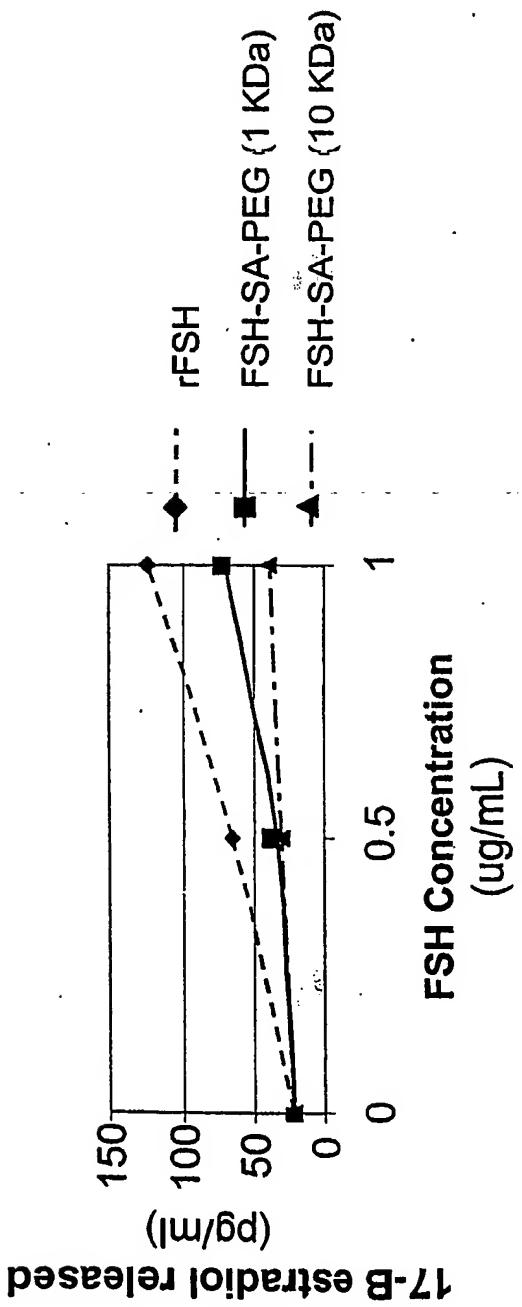
17-B estradiol released
(pg/ml)
150
100
50
0
0
0.5
1
FSH Concentration
(ug/mL)
rFSH
FSH-SA-PEG (1 KDa)
FSH-SA-PEG (10 KDa)

FIG. 170

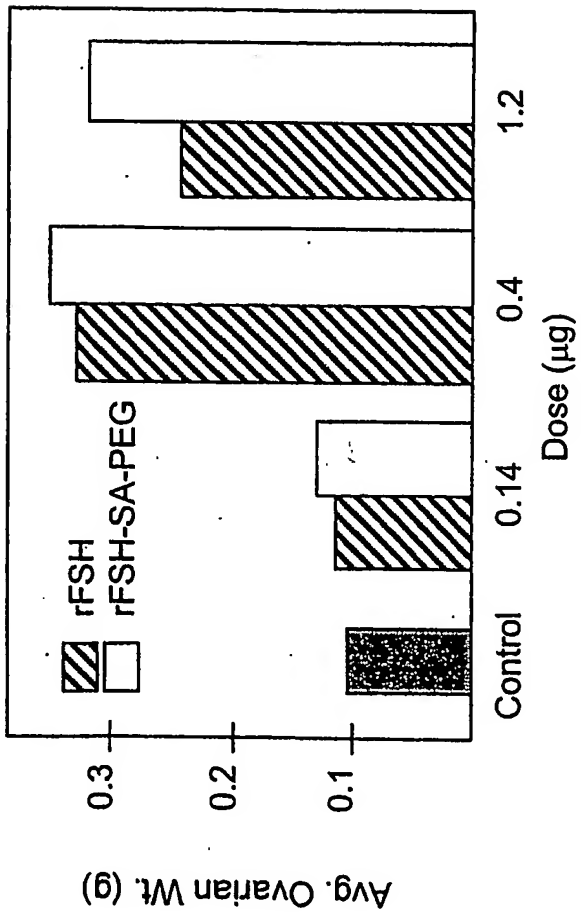
Avg. Ovarian Wt. (g)
0.3
0.2
0.1
rFSH
rFSH-SA-PEG
Control
0.14
0.4
1.2
Dose (µg)

FIG. 171

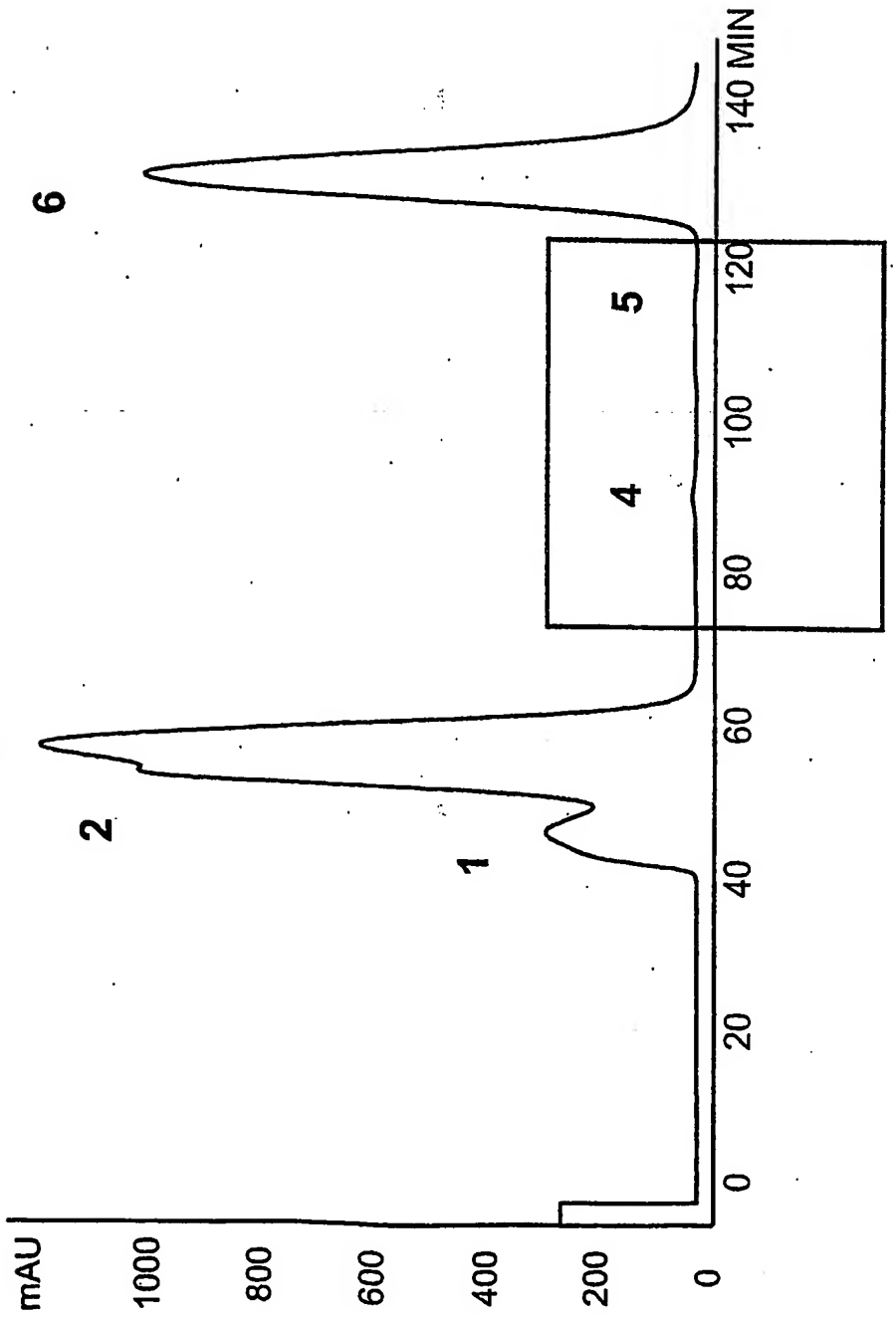

FIG. 172A

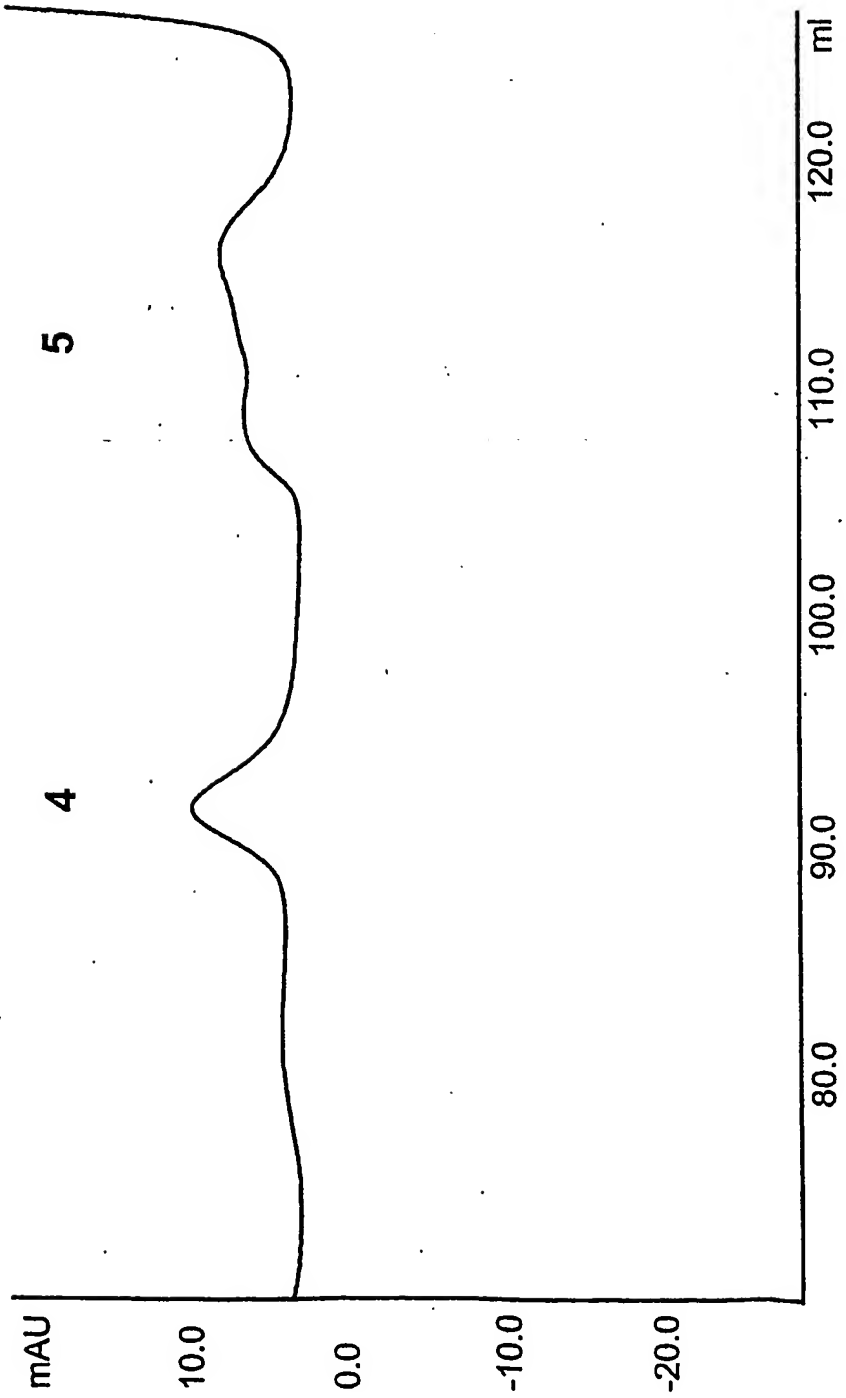

FIG. 172B

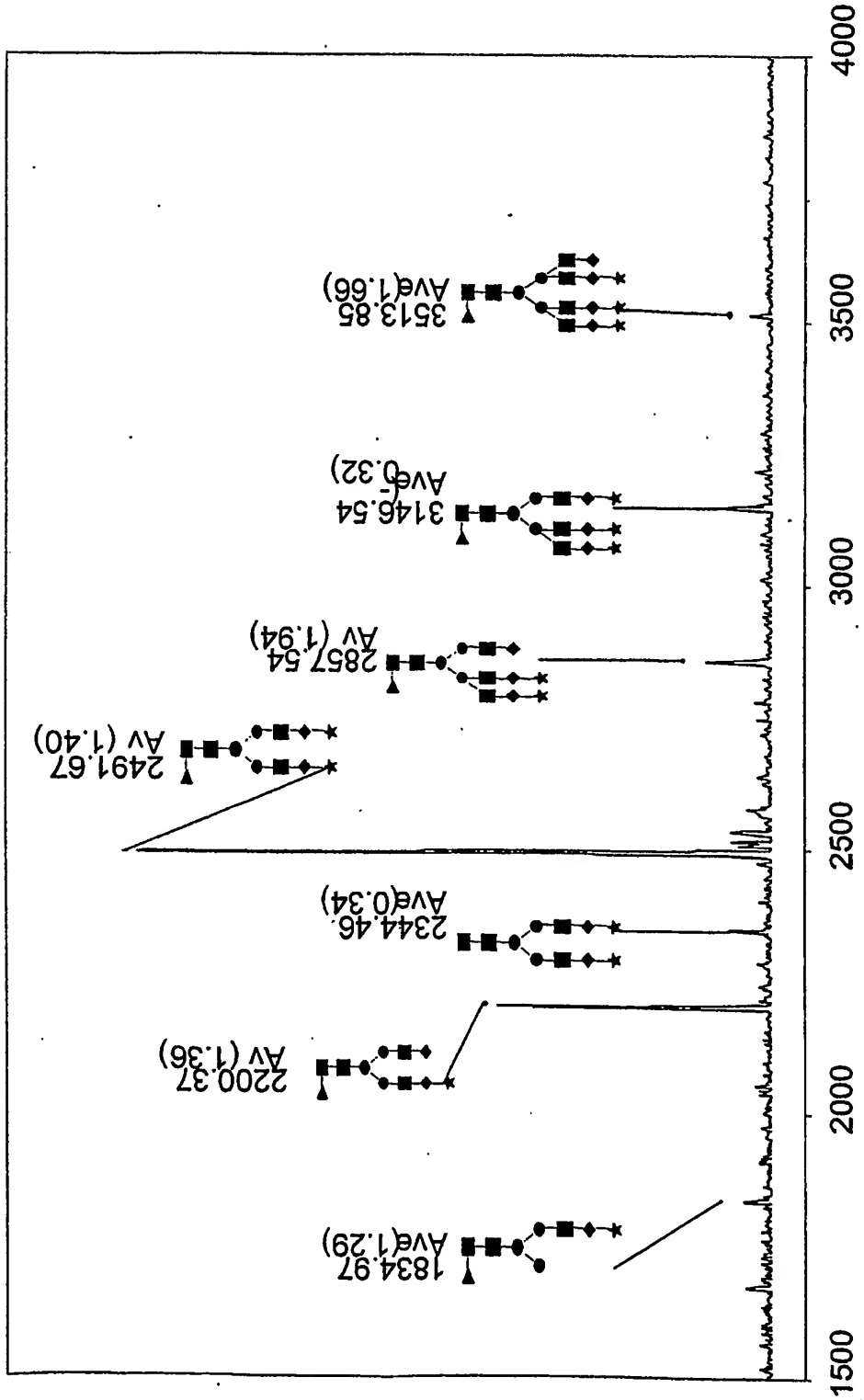
1834.97
Ave(1.29)
2200.37
Av (1.36)
2344.46
Ave(0.34)
2491.67
Av (1.40)
2857.54
Av (1.94)
3146.54
Ave(0.32)
3513.85
Ave(1.66)
1500
2000
2500
3000
3500
4000
m/z

FIG. 173A

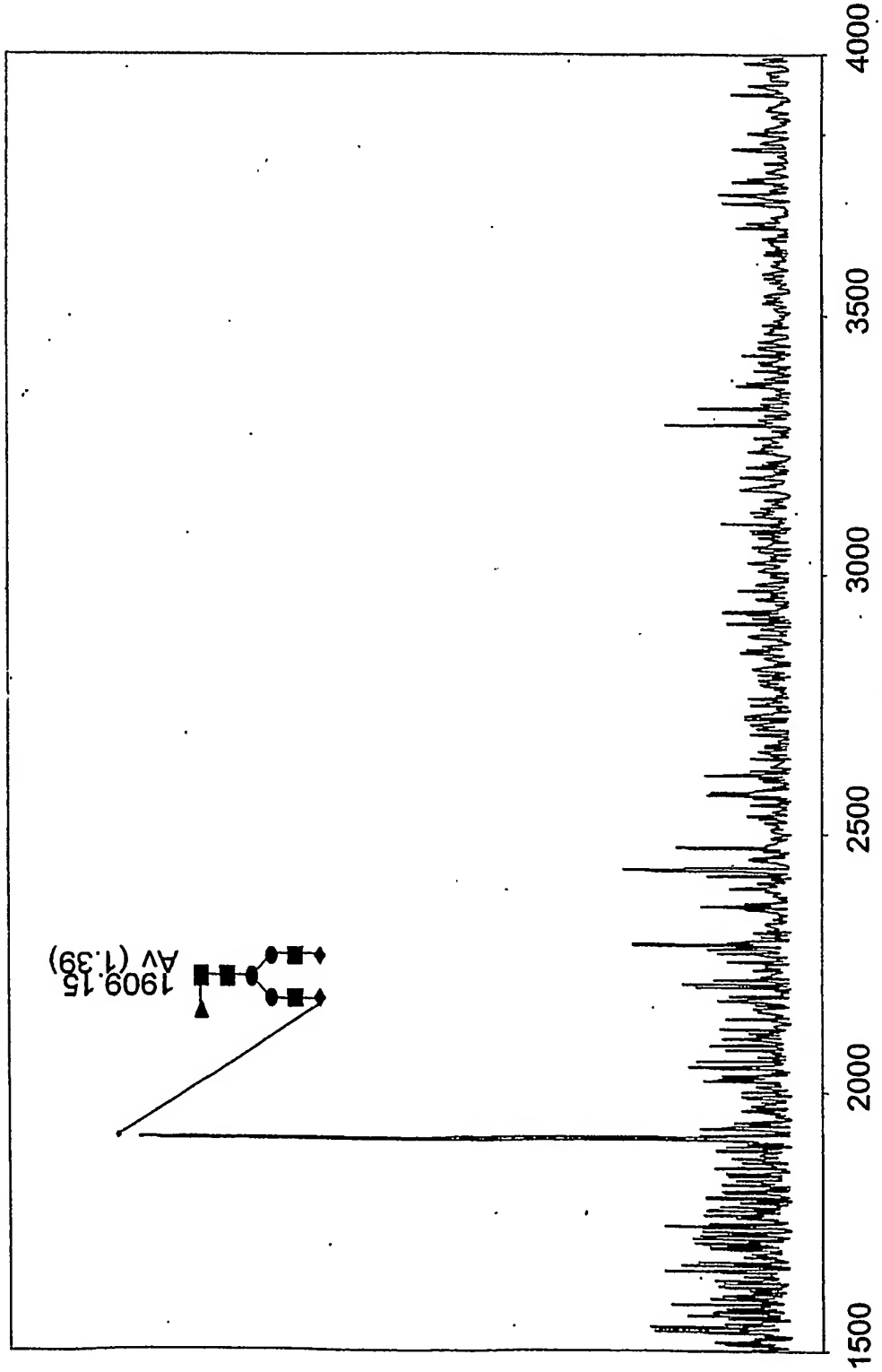

FIG. 173B

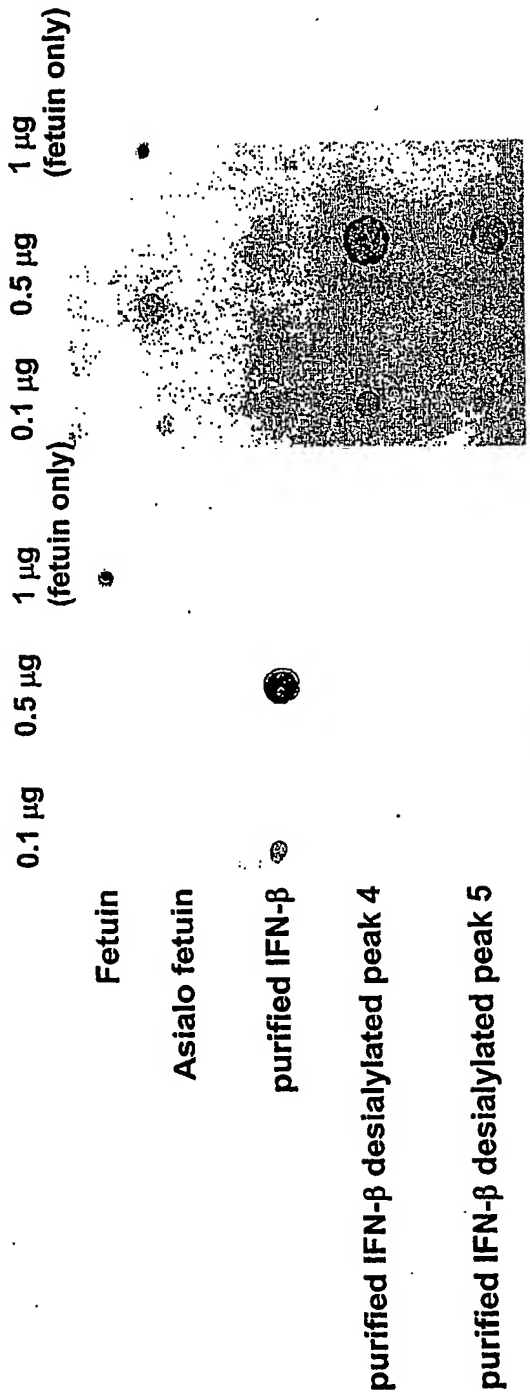
0.1 µg
0.5 µg
1 µg (fetuin only)
0.1 µg
0.5 µg
1 µg (fetuin only)
Fetuin
Asialo fetuin
purified IFN-β
purified IFN-β desialylated peak 4
purified IFN-β desialylated peak 5
MAA blot
ECL blot

FIG. 174

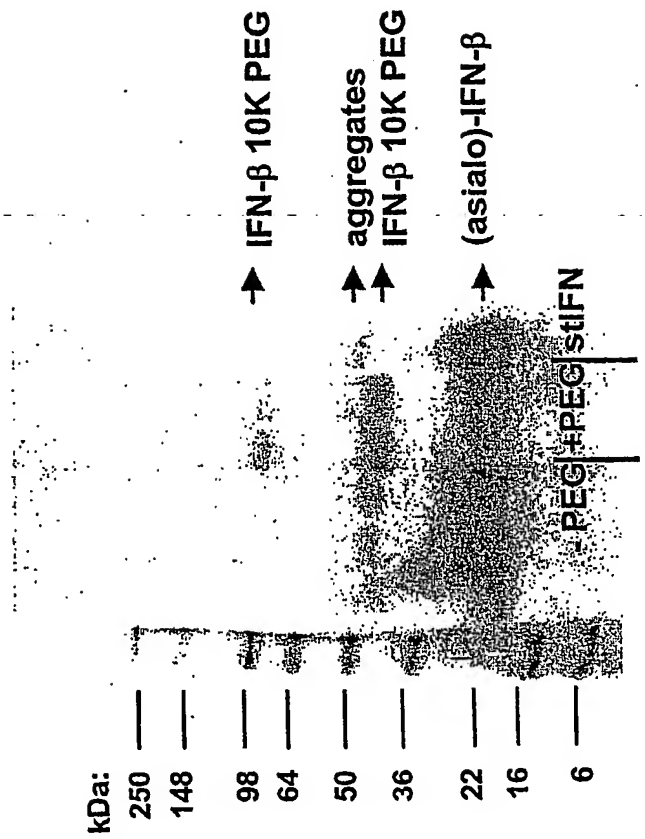
IFN-β 10K PEG
aggregates
IFN-β 10K PEG
(asialo)-IFN-β
PEG
+PEG
stIFN
kDa:
250
148
98
64
50
36
22
16
6

FIG. 175

FIG. 176

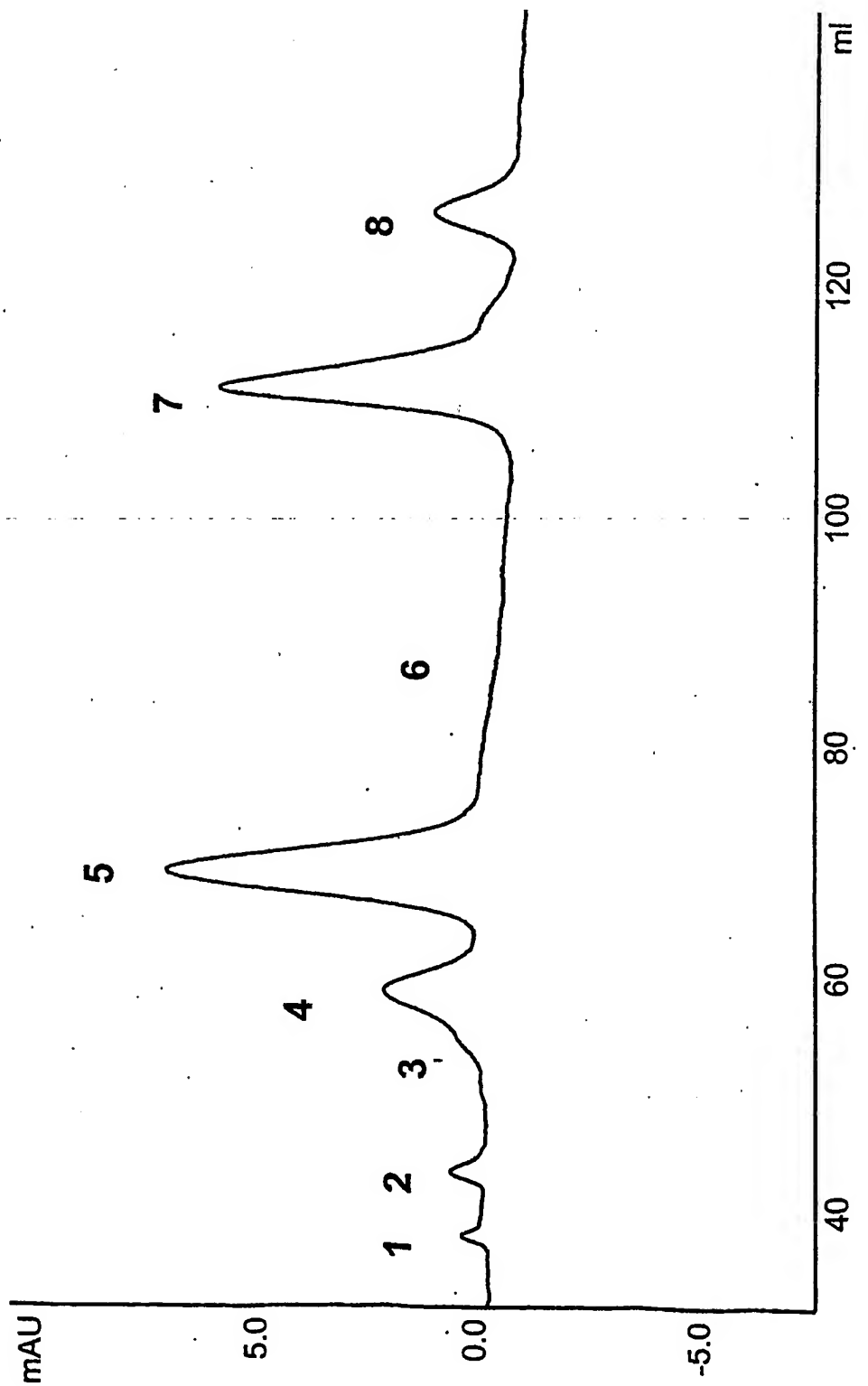

FIG. 177

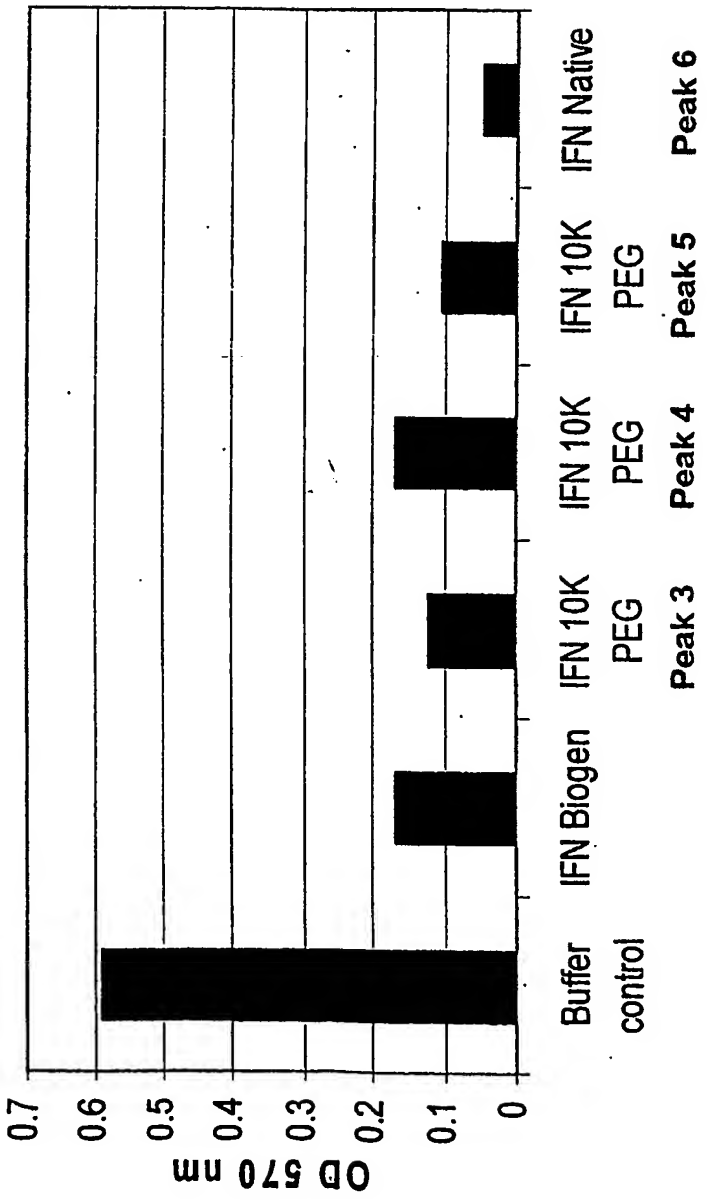
OD 570 nm
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Buffer control
IFN Biogen
IFN 10K PEG Peak 3
IFN 10K PEG Peak 4
IFN 10K PEG Peak 5
IFN Native Peak 6

FIG. 178

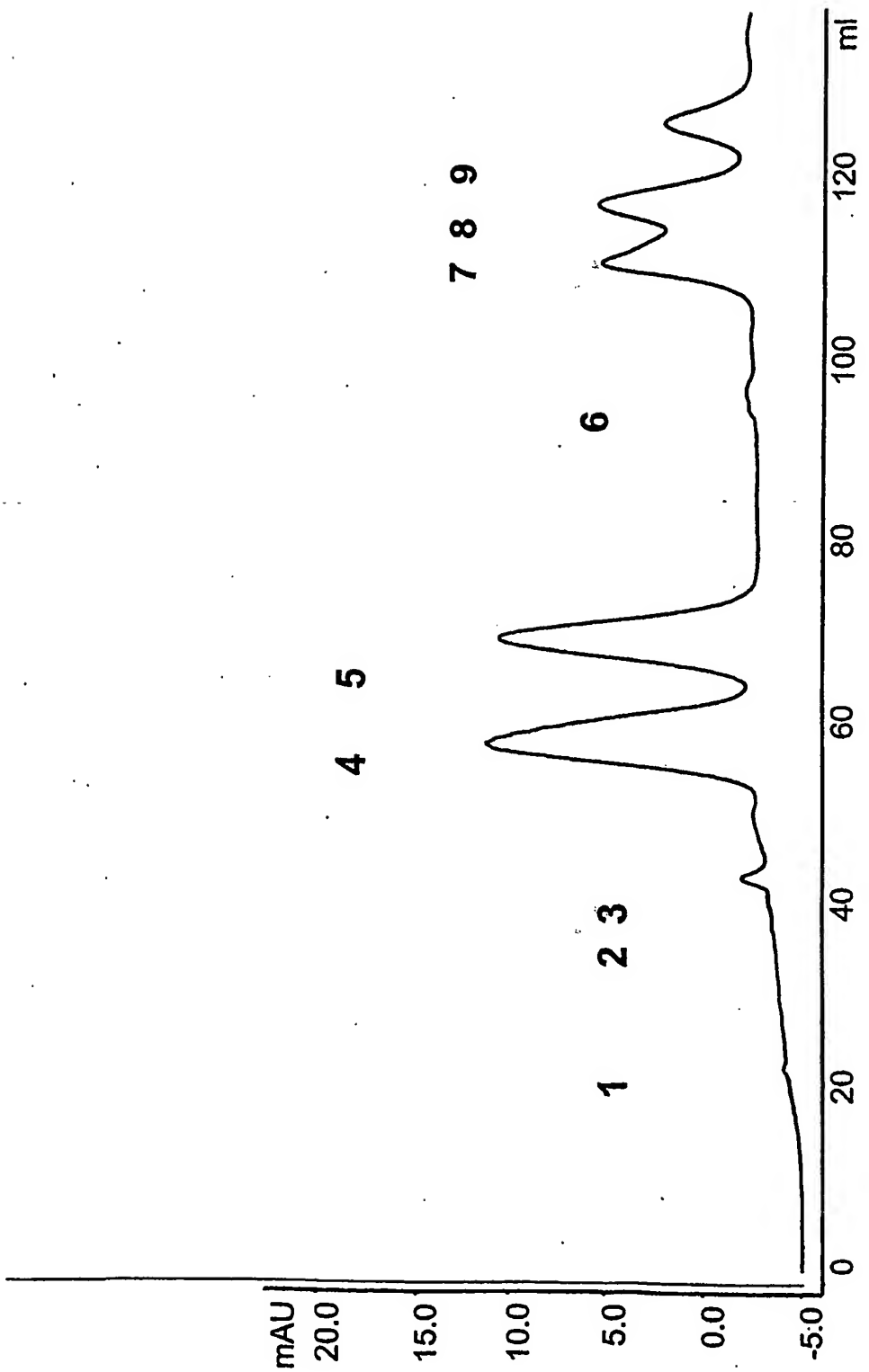

FIG. 179

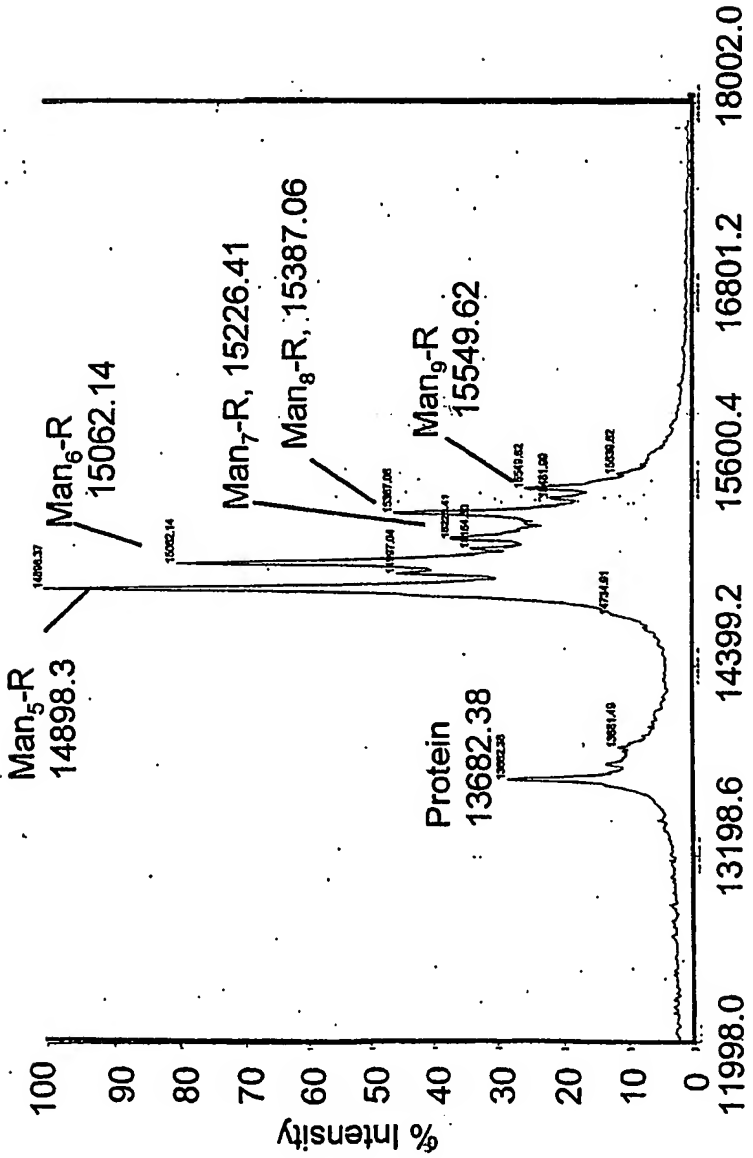
Man5-R
14898.3
Man6-R
15062.14
Man7-R, 15226.41
Man8-R, 15387.06
Man9-R
15549.62
Protein
13682.38
% Intensity
Mass (m/z)
11998.0
13198.6
14399.2
15600.4
16801.2
18002.0
0
10
20
30
40
50
60
70
80
90
100

FIG. 180A

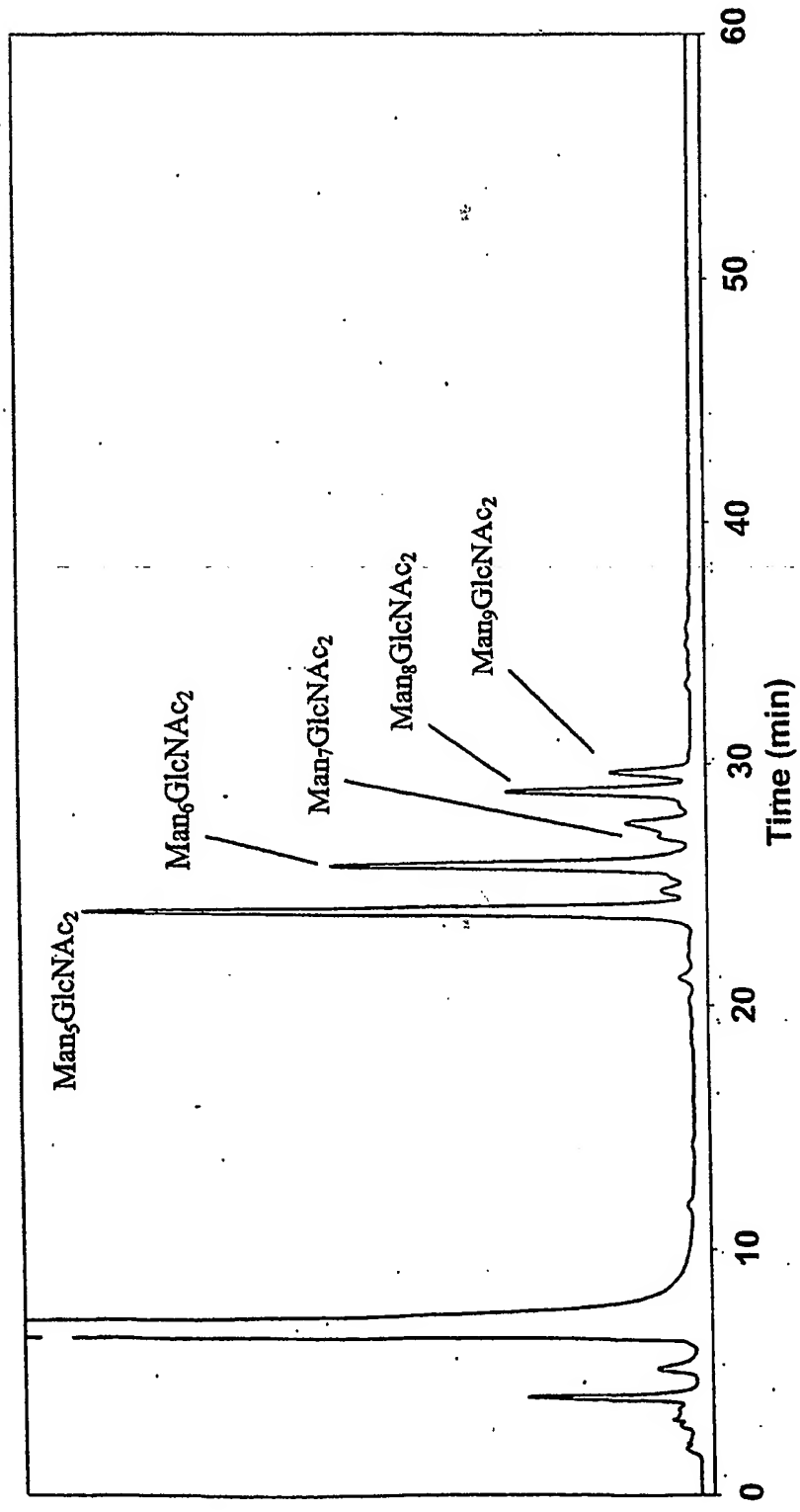
Man5GlcNAc2
Man6GlcNAc2
Man7GlcNAc2
Man8GlcNAc2
Man9GlcNAc2
0
10
20
30
40
50
60
Time (min)

FIG. 180B

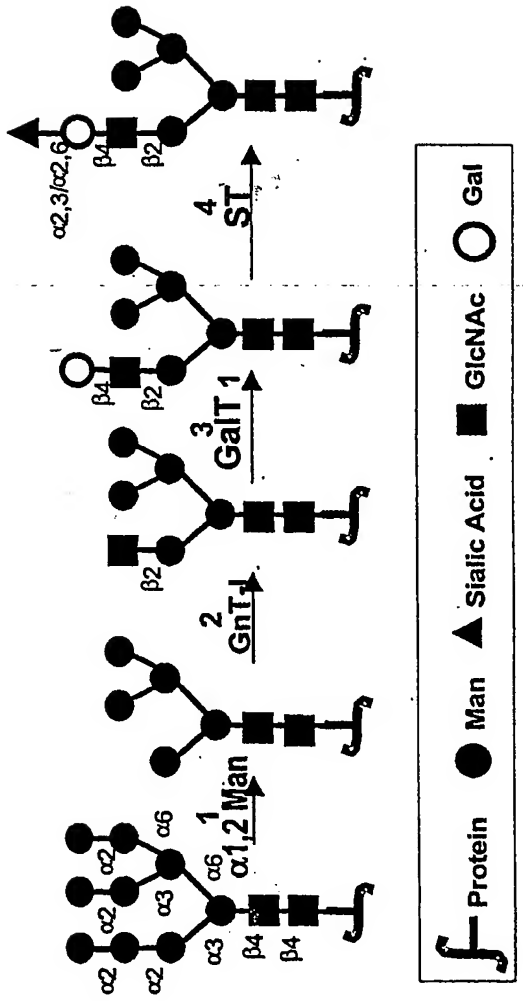
Protein
Man
Sialic Acid
GlcNAc
Gal
1
α1,2 Man
2
GnT I
3
GalT 1
4
ST
α2,3/α2,6
β4
β2
α6
α3
α2

FIG. 181

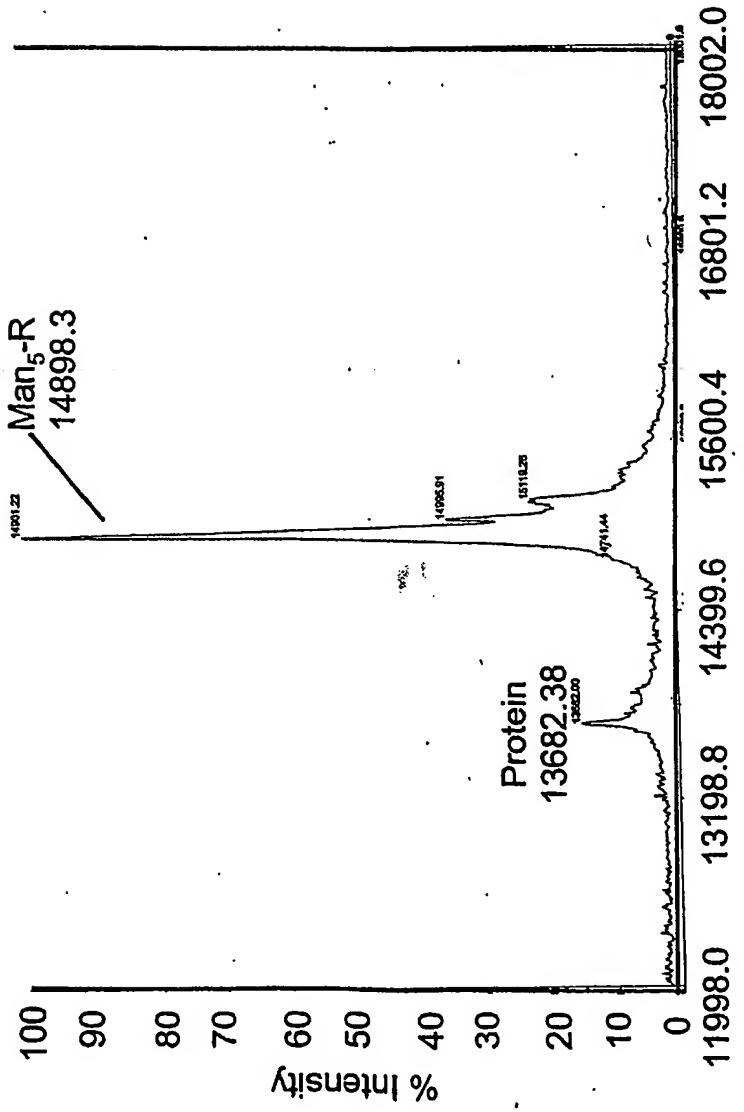
Man5-R
14898.3
Protein
13682.38
% Intensity
100
90
80
70
60
50
40
30
20
10
0
11998.0
13198.8
14399.6
15600.4
16801.2
18002.0
Mass (m/z)

FIG. 182A

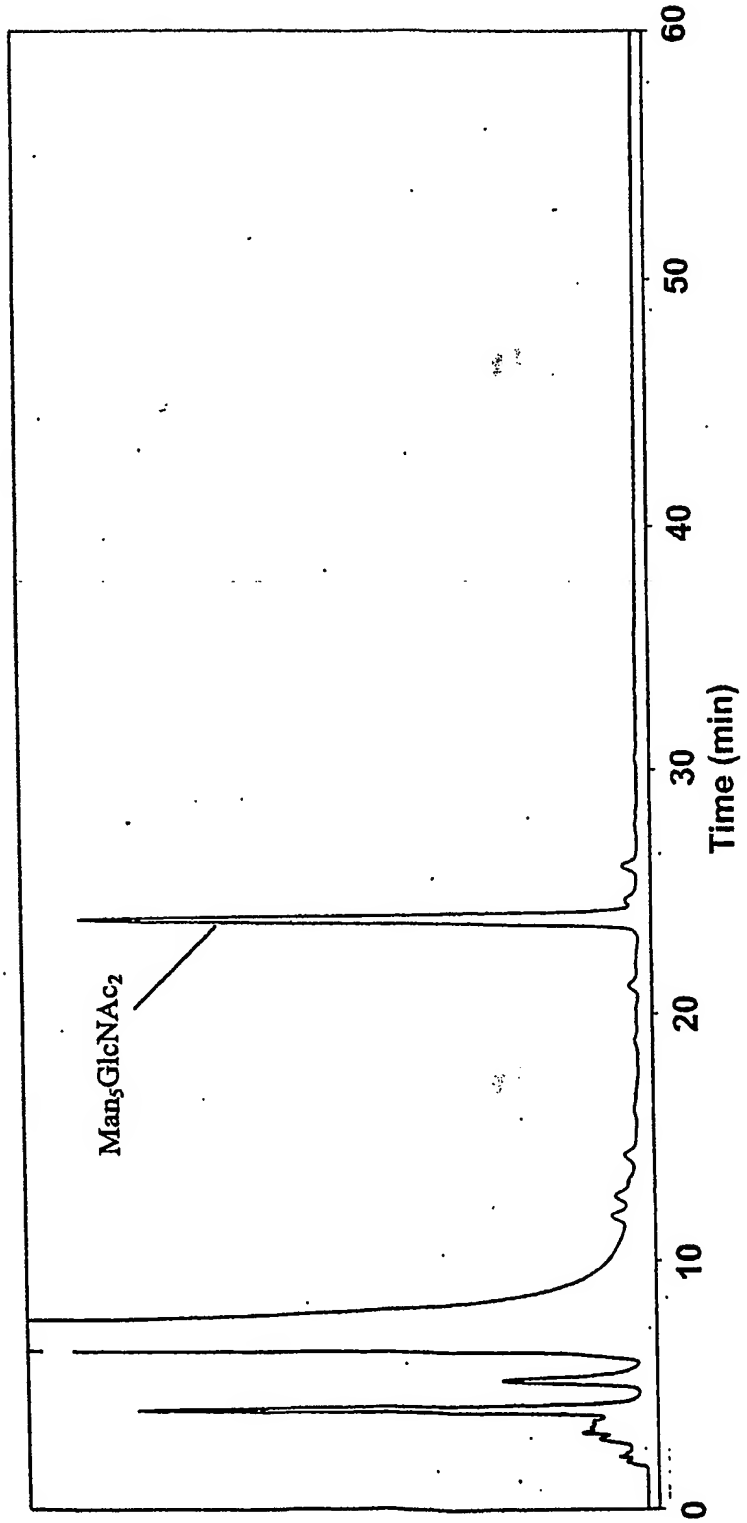

FIG. 182B

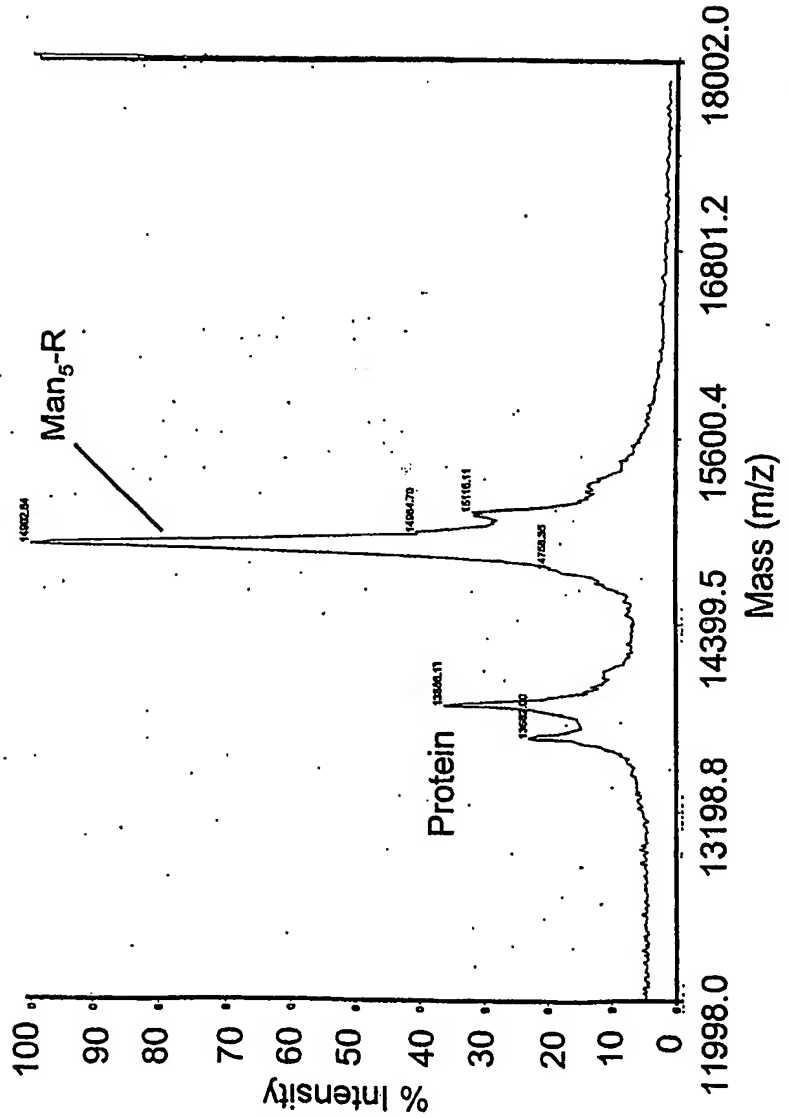
Man5-R
Protein
% Intensity
100
90
80
70
60
50
40
30
20
10
0
11998.0
13198.8
14399.5
15600.4
16801.2
18002.0
Mass (m/z)

FIG. 183

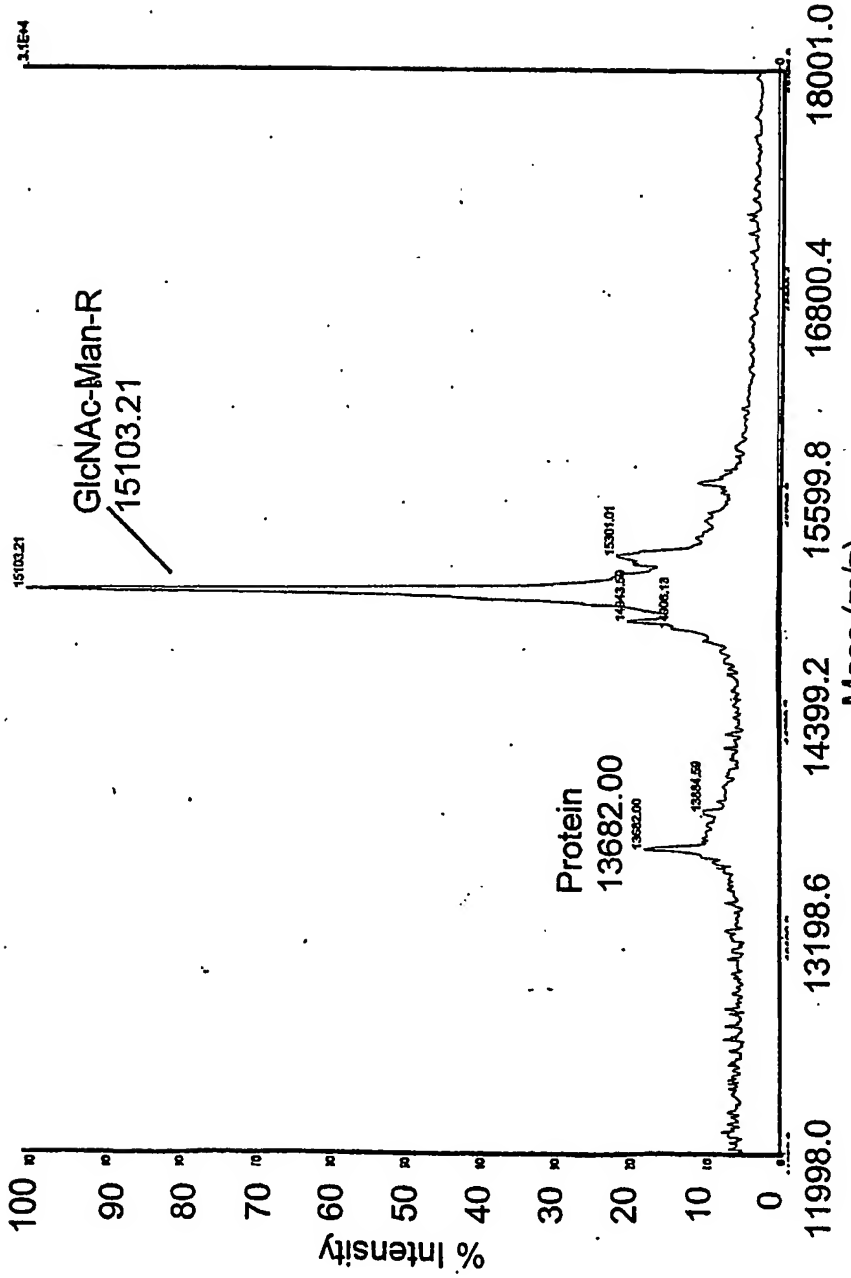
GlcNAc-Man-R
15103.21
Protein
13682.00
% Intensity
Mass (m/z)
11998.0
13198.6
14399.2
15599.8
16800.4
18001.0
0
10
20
30
40
50
60
70
80
90
100

FIG. 184

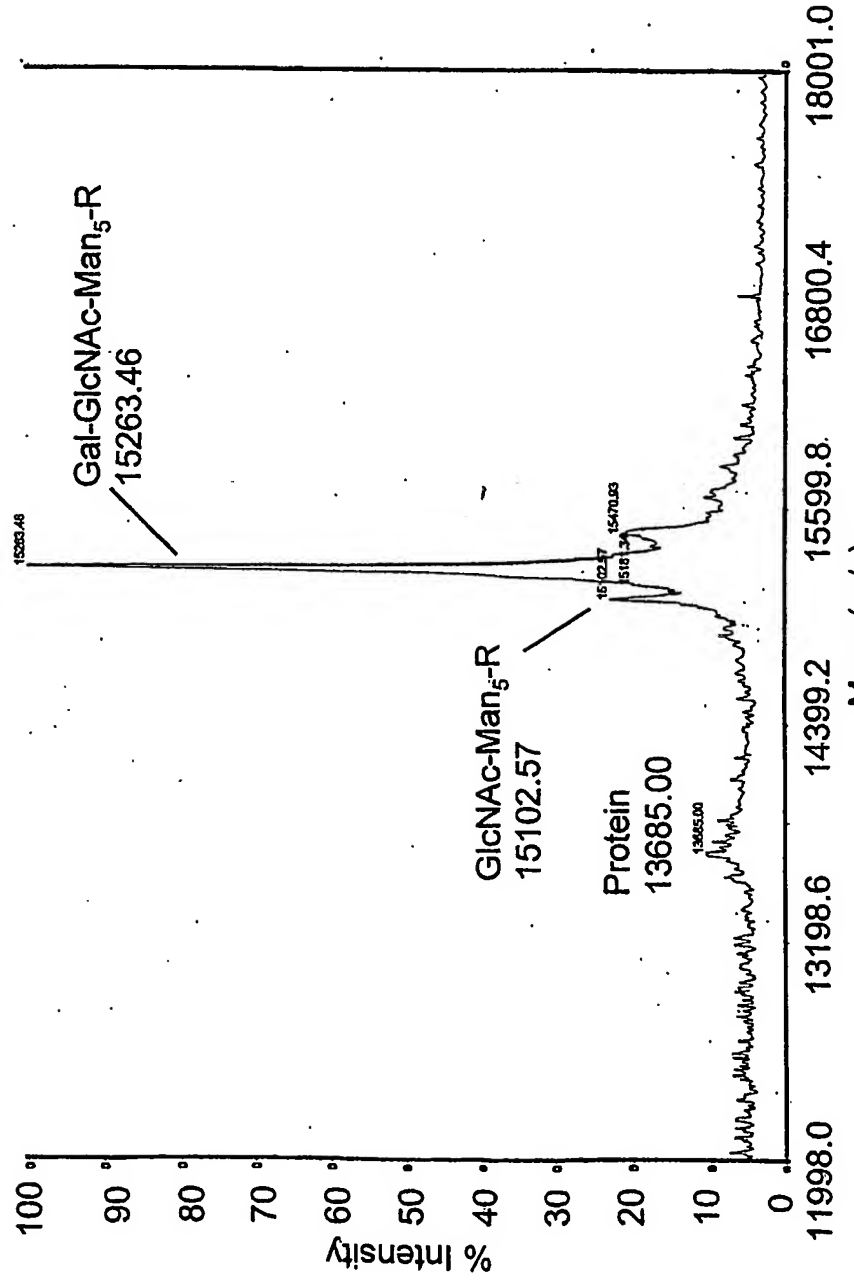
Gal-GlcNAc-Man5-R
15263.46
GlcNAc-Man5-R
15102.57
Protein
13685.00
% Intensity
100
90
80
70
60
50
40
30
20
10
0
11998.0
13198.6
14399.2
15599.8
16800.4
18001.0
Mass (m/z)

FIG. 185

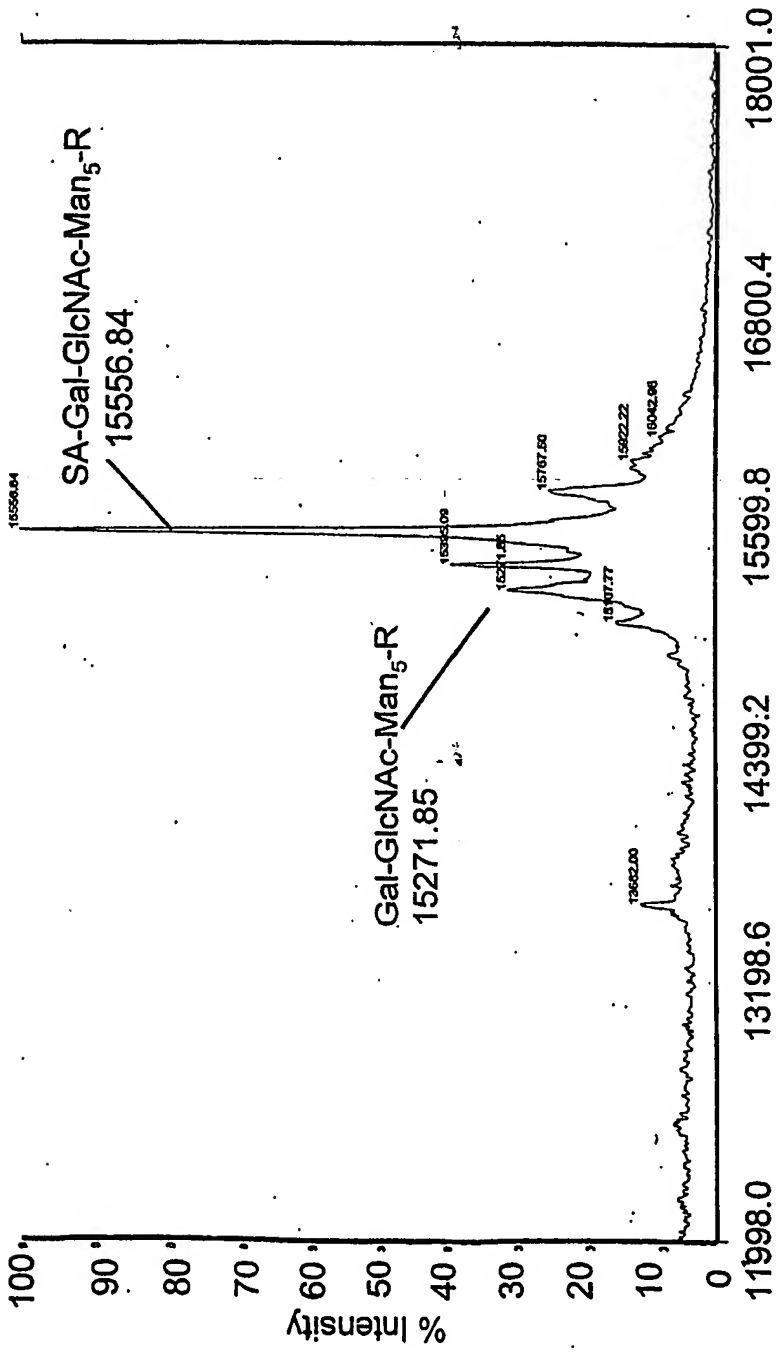
SA-Gal-GlcNAc-Man5-R
15556.84
Gal-GlcNAc-Man5-R
15271.85
% Intensity
Mass (m/z)
100
90
80
70
60
50
40
30
20
10
0
11998.0
13198.6
14399.2
15599.8
16800.4
18001.0

FIG. 186

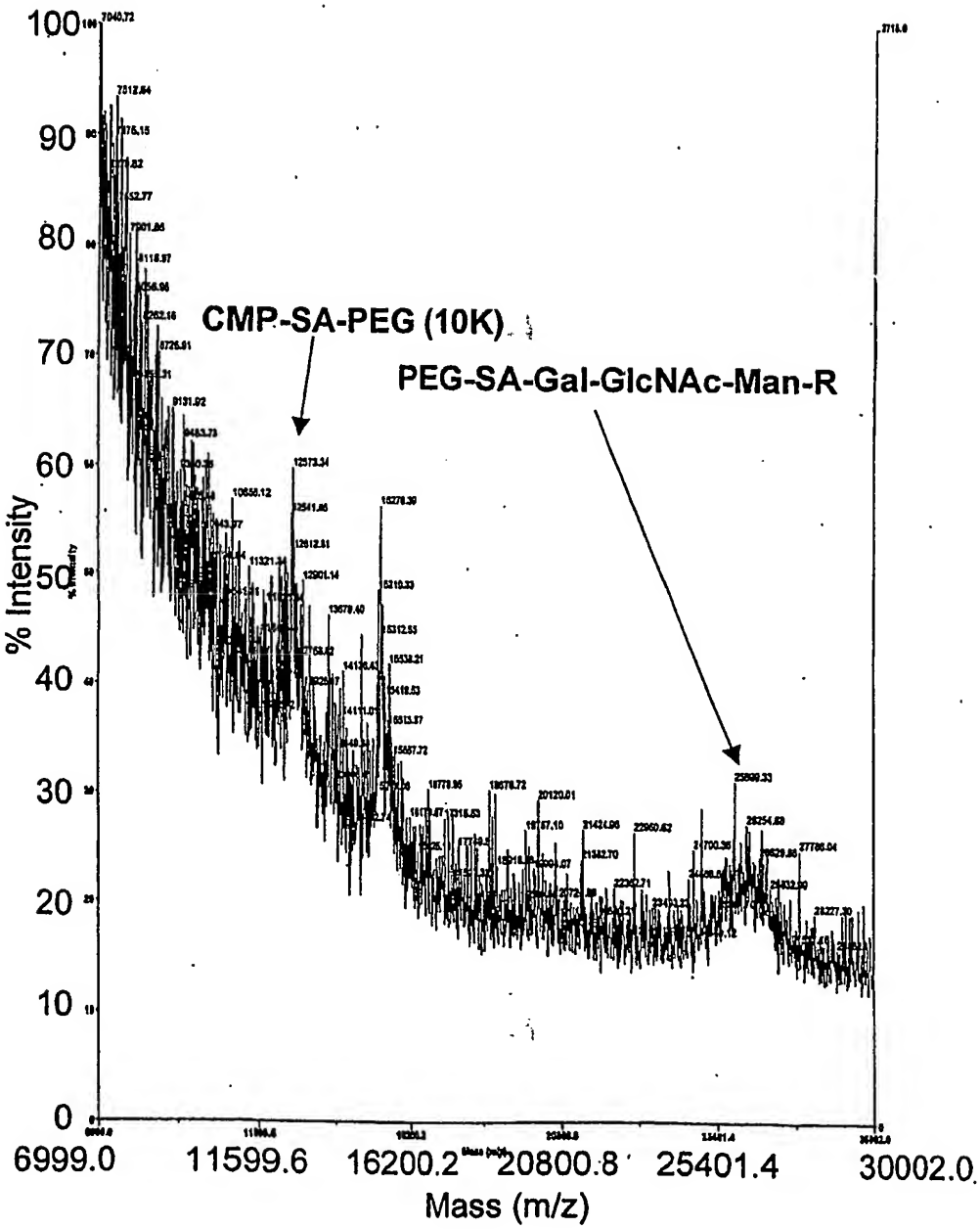
CMP-SA-PEG (10K)
PEG-SA-Gal-GlcNAc-Man-R
% Intensity
100
90
80
70
60
50
40
30
20
10
0
6999.0
11599.6
16200.2
20800.8
25401.4
30002.0
Mass (m/z)

FIG. 187A

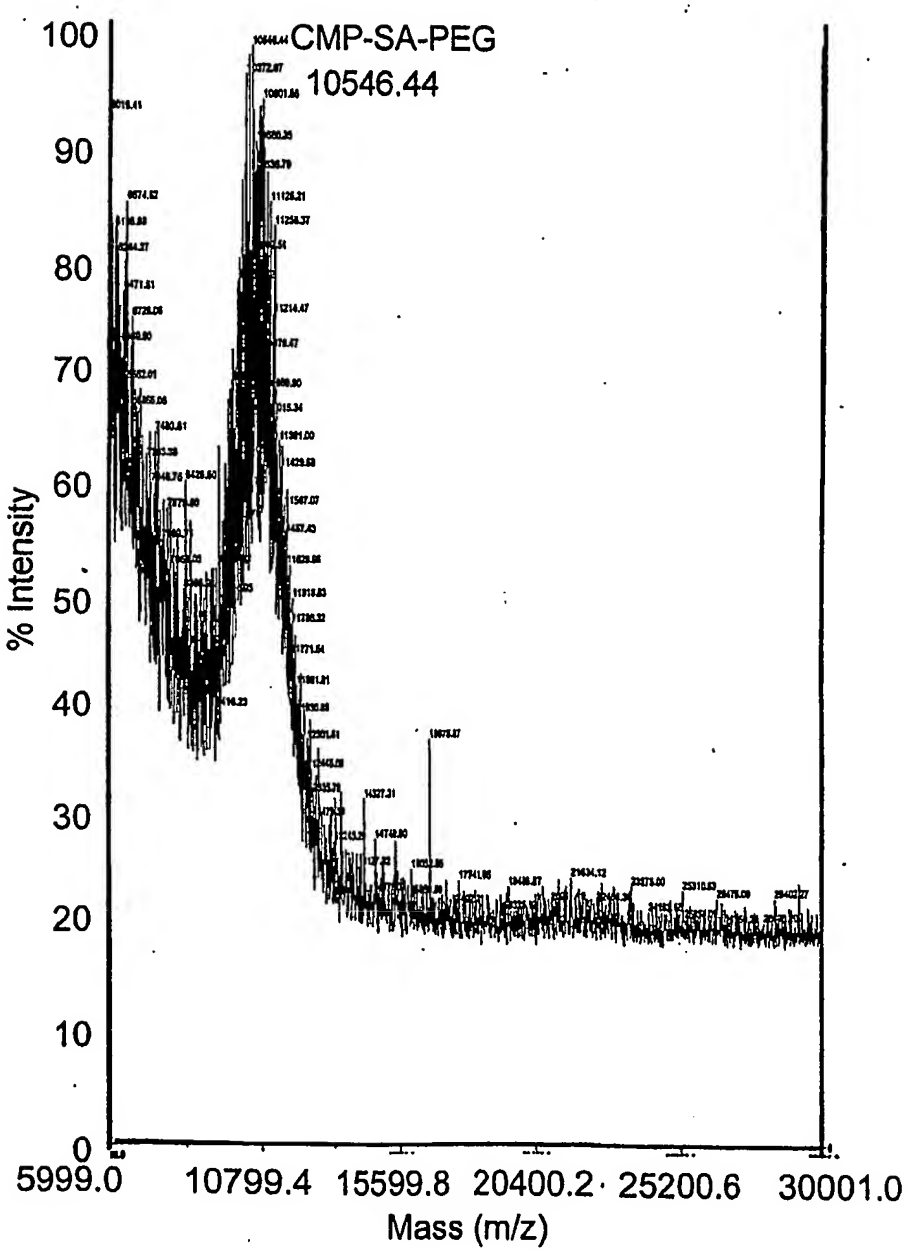
CMP-SA-PEG
10546.44
100
90
80
70
60
50
40
30
20
10
0
% Intensity
5999.0
10799.4
15599.8
20400.2
25200.6
30001.0
Mass (m/z)

FIG. 187B

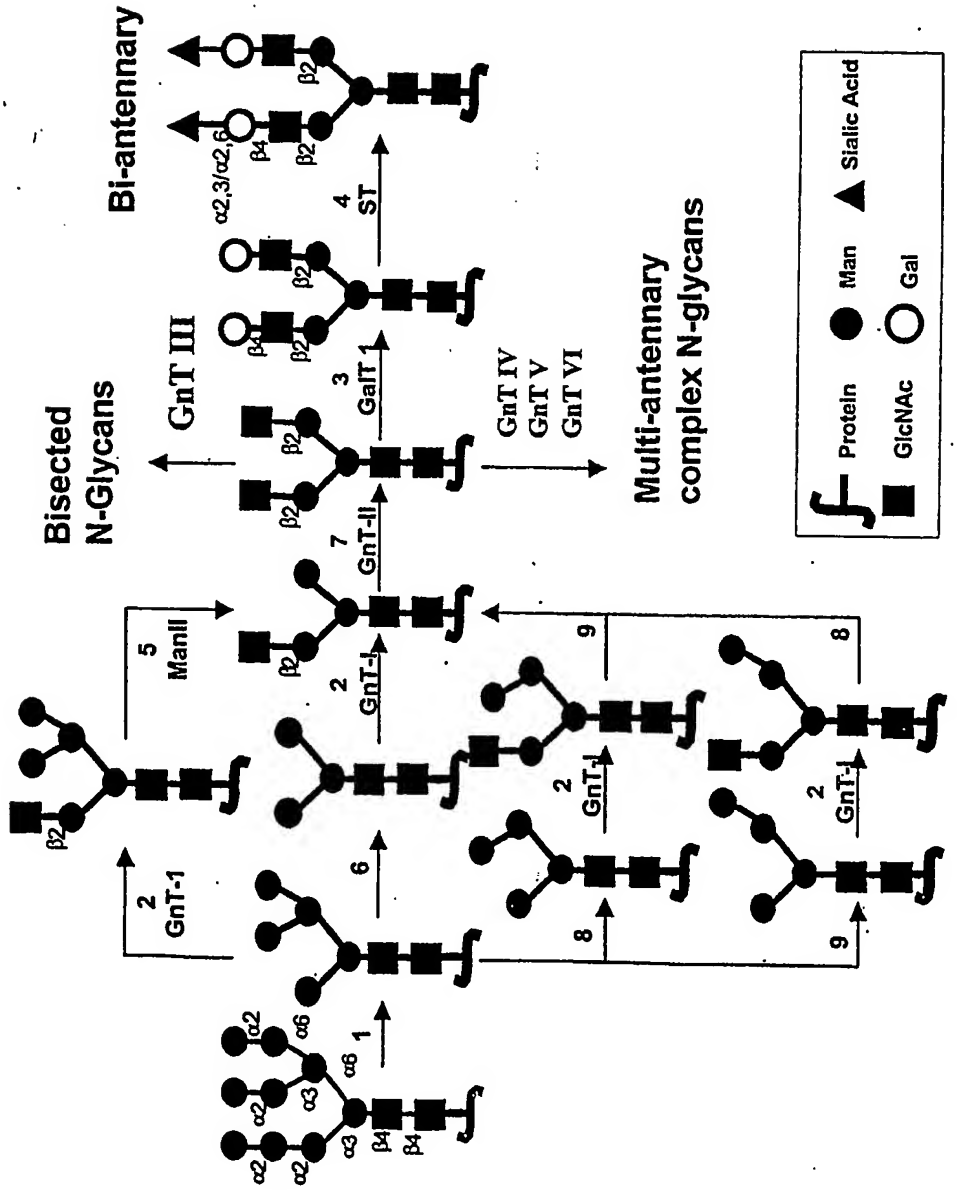
Bi-antennary
Bisected
N-Glycans
GnT III
Multi-antennary
complex N-glycans
GnT IV
GnT V
GnT VI
Protein
Man
Sialic Acid
GlcNAc
Gal
1
2 GnT-1
3 GalT 1
4 ST
5 ManII
6
7 GnT-II
8
9
2 GnT-I

FIG. 188

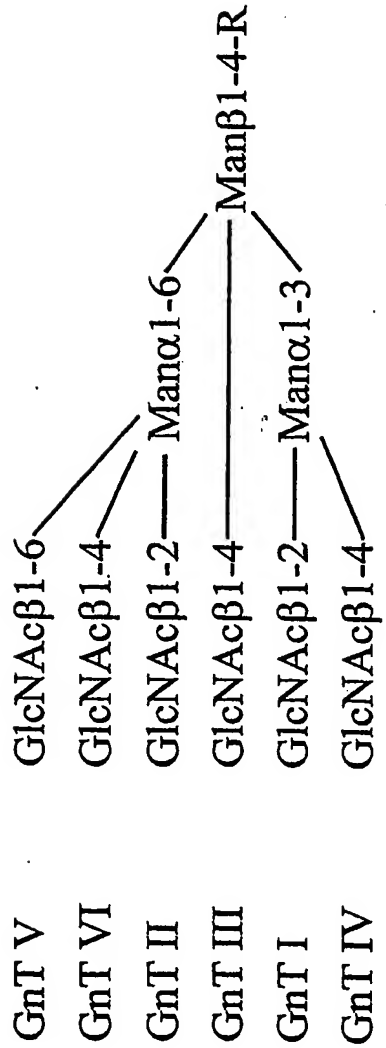
GnT V
GnT VI
GnT II
GnT III
GnT I
GnT IV
GlcNAcβ1-6
GlcNAcβ1-4
GlcNAcβ1-2
Manα1-6
GlcNAcβ1-4
Manβ1-4-R
GlcNAcβ1-2
Manα1-3
GlcNAcβ1-4

FIG. 189

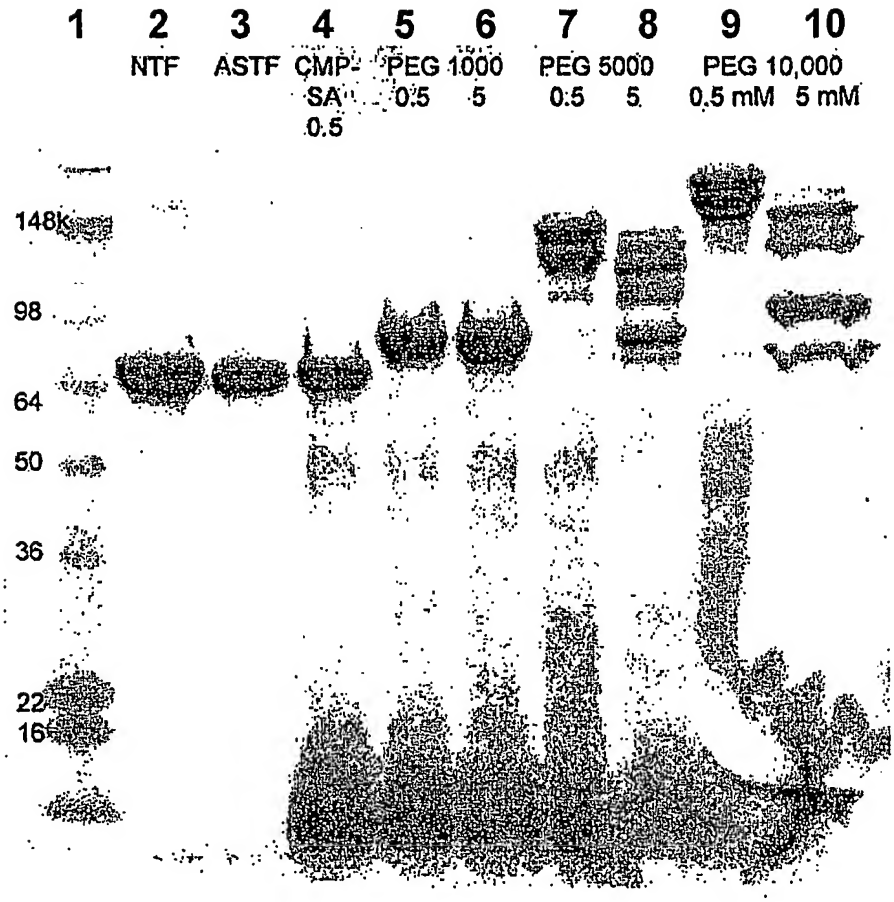
1
2
NTF
3
ASTF
4
CMP-SA 0.5
5
PEG 1000 0.5
6
5
7
PEG 5000 0.5
8
5
9
PEG 10,000 0.5 mM
10
5 mM
148K
98
64
50
36
22
16

FIG. 190

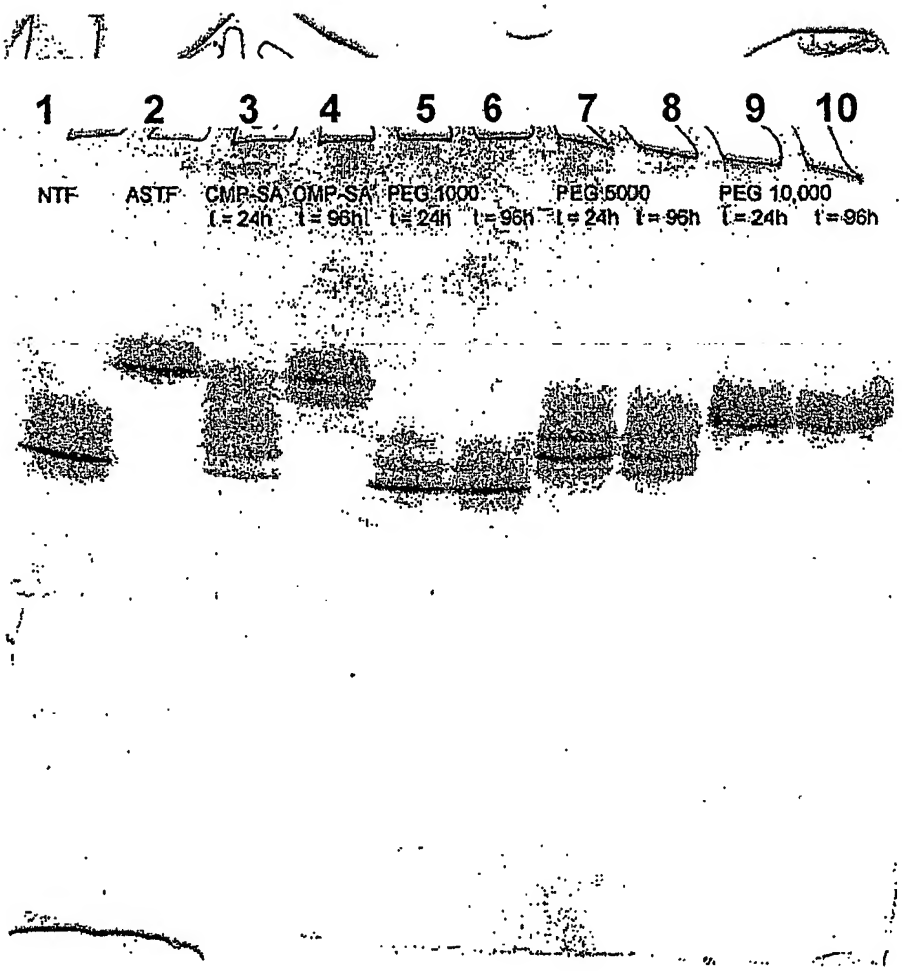
1 2 3 4 5 6 7 8 9 10
NTF
ASTF
CMP-SA t = 24h
CMP-SA t = 96h
PEG 1000 t = 24h
PEG 1000 t = 96h
PEG 5000 t = 24h
PEG 5000 t = 96h
PEG 10,000 t = 24h
PEG 10,000 t = 96h

FIG. 191

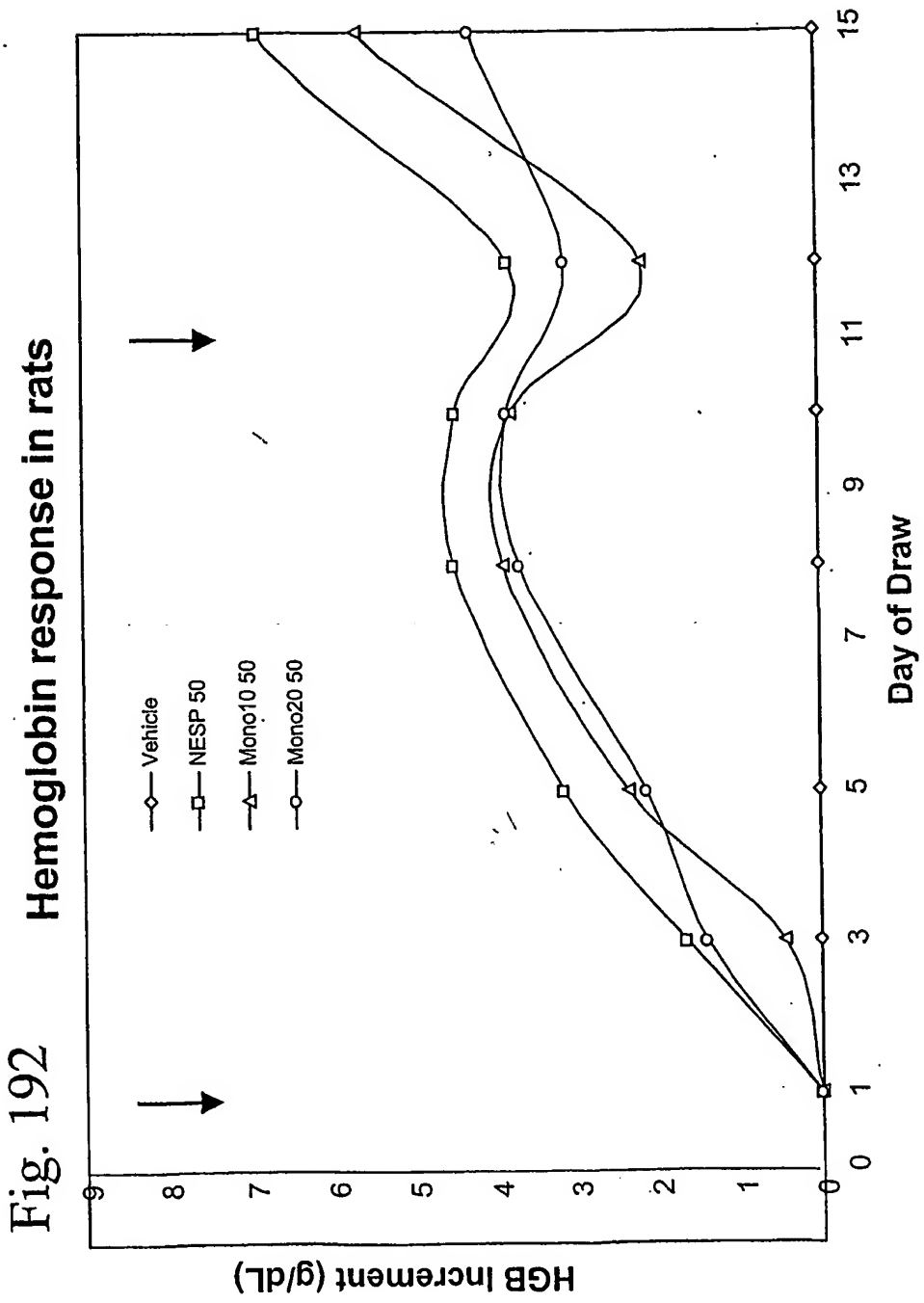
Hemoglobin response in rats
HGB Increment (g/dL)
Day of Draw
Vehicle
NESP 50
Mono10 50
Mono20 50
0
1
2
3
4
5
6
7
8
9
0
1
3
5
7
9
11
13
15

Fig. 192

SEQUENCE LISTING

<110> Neose Technologies, Inc.
DeFrees, Shawn
Zopf, David
Bayer, Robert
Hakes, David
Chen, Xi
Bowe, Caryne

<120> ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF ERYTHROPOIETIN

<130> 040853-01-5083WO

<150> PCT/US02/32263
<151> 2002-10-09

<150> US 10/287,994
<151> 2002-11-5

<150> US 10/360,770
<151> 2003-01-06

<150> US 10/369,779
<151> 2003-03-17

<150> US 10/410,945
<151> 2003-04-09

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<170> PatentIn version 3.2

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ctgtgccacc ccgaggagct ggtgctgctc ggacactctc tgggcatccc ctgggctccc 180

ctgagcagct gccccagcca ggccctgcag ctggcaggct gcttgagcca actccatagc 240

ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc cgagttgggt 300

cccaccttgg acacactgca gctggacgtc gccgactttg ccaccaccat ctggcagcag 360

atggaagaac tgggaatggc ccctgccctg cagcccaccc agggtgccat gccggccttc 420

gcctctgctt tccagcgccg ggcaggaggg gtcctggttg cctcccatct gcagagcttc 480

ctggaggtgt cgtaccgcgt tctacgccac cttgcccagc cctga 525

<210> 2
<211> 174
<212> PRT

<213> Homo sapiens

<400> 2

```
Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1               5                  10                  15

Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
            20                  25                  30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
        35                  40                  45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
    50                  55                  60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65                  70                  75                  80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                85                  90                  95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
            100                 105                 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
        115                 120                 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
    130                 135                 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
145                 150                 155                 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170
```

<210> 3
<211> 1733
<212> DNA
<213> Homo sapiens

<400> 3

```
gcgcctctta tgtacccaca aaaatctatt ttcaaaaaag ttgctctaag aatatagtta    60

tcaagttaag taaaatgtca atagcctttt aatttaattt ttaattgttt tatcattctt   120

tgcaataata aaacattaac tttatacttt ttaatttaat gtatagaata gagatataca   180

taggatatgt aaatagatac acagtgtata tgtgattaaa atataatggg agattcaatc   240

agaaaaaagt ttctaaaaag gctctggggt aaaagaggaa ggaaacaata atgaaaaaaa   300

tgtggtgaga aaaacagctg aaaacccatg taaagagtgt ataaagaaag caaaaagaga   360

agtagaaagt aacacagggg catttggaaa atgtaaacga gtatgttccc tatttaaggc   420

taggcacaaa gcaaggtctt cagagaacct ggagcctaag gtttaggctc acccatttca   480

accagtctag cagcatctgc aacatctaca atggccttga cctttgcttt actggtggcc   540

ctcctggtgc tcagctgcaa gtcaagctgc tctgtgggct gtgatctgcc tcaaacccac   600
```

agcctgggta gcaggaggac cttgatgctc ctggcacaga tgaggagaat ctctcttttc 660

tcctgcttga aggacagaca tgactttgga tttccccagg aggagtttgg caaccagttc 720

caaaaggctg aaaccatccc tgtcctccat gagatgatcc agcagatctt caatctcttc 780

agcacaaagg actcatctgc tgcttgggat gagaccctcc tagacaaatt ctacactgaa 840

ctctaccagc agctgaatga cctggaagcc tgtgtgatac agggggtggg ggtgacagag 900

actcccctga tgaaggagga ctccattctg gctgtgagga aatacttcca aagaatcact 960

ctctatctga aagagaagaa atacagccct tgtgcctggg aggttgtcag agcagaaatc 1020

atgagatctt tttctttgtc aacaaacttg caagaaagtt taagaagtaa ggaatgaaaa 1080

ctggttcaac atggaaatga ttttcattga ttcgtatgcc agctcacctt tttatgatct 1140

gccatttcaa agactcatgt ttctgctatg accatgacac gatttaaatc ttttcaaatg 1200

tttttaggag tattaatcaa cattgtattc agctcttaag gcactagtcc cttacagagg 1260

accatgctga ctgatccatt atctatttaa atatttttaa aatattattt atttaactat 1320

ttataaaaca acttattttt gttcatatta tgtcatgtgc acctttgcac agtggttaat 1380

gtaataaaat gtgttctttg tatttggtaa atttattttg tgttgttcat tgaacttttg 1440

ctatggaact tttgtacttg tttattcttt aaaatgaaat tccaagccta attgtgcaac 1500

ctgattacag aataactggt acacttcatt tgtccatcaa tattatattc aagatataag 1560

taaaaataaa ctttctgtaa accaagttgt atgttgtact caagataaca gggtgaacct 1620

aacaaataca attctgctct cttgtgtatt tgatttttgt atgaaaaaaa ctaaaaatgg 1680

taatcatact taattatcag ttatggtaaa tggtatgaag agaagaagga acg 1733

<210> 4
<211> 188
<212> PRT
<213> Homo sapiens

<400> 4

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
1 5 10 15

Lys Ser Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu
20 25 30

Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
35 40 45

Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
50 55 60

Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
65 70 75 80

Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser

85 90 95

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
100 105 110

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
115 120 125

Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
130 135 140

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
145 150 155 160

Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
165 170 175

Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
180 185

<210> 5
<211> 757
<212> DNA
<213> Homo sapiens

<400> 5
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tccatgagct acaacttgct tggattccta caaagaagca gcaattttca gtgtcagaag 120

ctcctgtggc aattgaatgg gaggcttgaa tattgcctca aggacaggat gaactttgac 180

atccctgagg agattaagca gctgcagcag ttccagaagg aggacgccgc attgaccatc 240

tatgagatgc tccagaacat ctttgctatt ttcagacaag attcatctag cactggctgg 300

aatgagacta ttgttgagaa cctcctggct aatgtctatc atcagataaa ccatctgaag 360

acagtcctgg aagaaaaact ggagaaagaa gattttacca ggggaaaact catgagcagt 420

ctgcacctga aaagatatta tgggaggatt ctgcattacc tgaaggccaa ggagtacagt 480

cactgtgcct ggaccatagt cagagtggaa atcctaagga acttttactt cattaacaga 540

cttacaggtt acctccgaaa ctgaagatct cctagcctgt ccctctggga ctggacaatt 600

gcttcaagca ttcttcaacc agcagatgct gtttaagtga ctgatggcta atgtactgca 660

aatgaaagga cactagaaga ttttgaaatt tttattaaat tatgagttat ttttatttat 720

ttaaatttta ttttggaaaa taaattattt ttggtgc 757

<210> 6
<211> 187
<212> PRT
<213> Homo sapiens

<400> 6
Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
1 5 10 15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
85 90 95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
100 105 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145 150 155 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
180 185

<210> 7
<211> 1332
<212> DNA
<213> Homo sapiens

<400> 7
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gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc 180

tccttcgagg aggcccggga gatcttcaag gacgcggaga ggacgaagct gttctggatt 240

tcttacagtg atggggacca gtgtgcctca agtccatgcc agaatggggg ctcctgcaag 300

gaccagctcc agtcctatat ctgcttctgc ctccctgcct tcgagggccg gaactgtgag 360

acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggctgtga gcagtactgc 420

agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgctggca 480

gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa 540

aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg 600

gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg 660

atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg 720

aacctgatcg cggtgctggg cgagcacgac ctcagcgagc acgacgggga tgagcagagc 780

cggcgggtgg cgcaggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac 840

atcgcgctgc tccgcctgca ccagcccgtg gtcctcactg accatgtggt gcccctctgc 900

ctgcccgaac ggacgttctc tgagaggacg ctggccttcg tgcgcttctc attggtcagc 960

ggctggggcc agctgctgga ccgtggcgcc acggccctgg agctcatggt gctcaacgtg 1020

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agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctcccag 1260

tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gcccaggagt cctcctgcga 1320

gccccatttc cc 1332

<210> 8
<211> 444
<212> PRT
<213> Homo sapiens

<400> 8
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
1 5 10 15
Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
20 25 30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225 230 235 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
245 250 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
260 265 270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
290 295 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305 310 315 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
325 330 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
340 345 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
355 360 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
370 375 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385 390 395 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
405 410 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
420 425 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
435 440

<210> 9
<211> 1437
<212> DNA
<213> Homo sapiens

<400> 9
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ggatatctac tcagtgctga atgtacagtt tttcttgatc atgaaaacgc caacaaaatt 120

ctgaatcggc caaagaggta taattcaggt aaattggaag agtttgttca agggaacctt 180

gagagagaat gtatggaaga aaagtgtagt tttgaagaac cacgagaagt ttttgaaaac 240

actgaaaaga caactgaatt ttggaagcag tatgttgatg gagatcagtg tgagtccaat 300

ccatgtttaa atggcggcag ttgcaaggat gacattaatt cctatgaatg ttggtgtccc 360

tttggatttg aaggaaagaa ctgtgaatta gatgtaacat gtaacattaa gaatggcaga 420

tgcgagcagt tttgtaaaaa tagtgctgat aacaaggtgg tttgctcctg tactgaggga 480

tatcgacttg cagaaaacca gaagtcctgt gaaccagcag tgccatttcc atgtggaaga 540

gtttctgttt cacaaacttc taagctcacc cgtgctgagg ctgtttttcc tgatgtggac 600

tatgtaaatc ctactgaagc tgaaaccatt ttggataaca tcactcaagg cacccaatca 660

tttaatgact tcactcgggt tgttggtgga gaagatgcca aaccaggtca attcccttgg 720

caggttgttt tgaatggtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa 780

tggattgtaa ctgctgccca ctgtgttgaa actggtgtta aaattacagt tgtcgcaggt 840

gaacataata ttgaggagac agaacataca gagcaaaagc gaaatgtgat tcgagcaatt 900

attcctcacc acaactacaa tgcagctatt aataagtaca accatgacat tgcccttctg 960

gaactggacg aacccttagt gctaaacagc tacgttacac ctatttgcat tgctgacaag 1020

gaatacacga acatcttcct caaatttgga tctggctatg taagtggctg ggcaagagtc 1080

ttccacaaag ggagatcagc tttagttctt cagtacctta gagttccact tgttgaccga 1140

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catgaaggag gtagagattc atgtcaagga gatagtgggg gaccccatgt tactgaagtg 1260

gaagggacca gtttcttaac tggaattatt agctggggtg aagagtgtgc aatgaaaggc 1320

aaatatggaa tatataccaa ggtatcccgg tatgtcaact ggattaagga aaaaacaaag 1380

ctcacttaat gaaagatgga tttccaaggt taattcattg gaattgaaaa ttaacag 1437

<210> 10
<211> 462
<212> PRT
<213> Homo sapiens

<400> 10
Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr
1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys

50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn
65 70 75 80

Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
145 150 155 160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
165 170 175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
180 185 190

Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu
195 200 205

Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe
210 215 220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
225 230 235 240

Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
245 250 255

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
260 265 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
275 280 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His
290 295 300

Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu
305 310 315 320

Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys
325 330 335

Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
340 345 350

Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu
355 360 365

Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu
370 375 380

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Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
385                 390                 395                 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
                405                 410                 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
            420                 425                 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
        435                 440                 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
    450                 455                 460
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<210> 11
<211> 603
<212> DNA
<213> Homo sapiens

<400> 11

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atggattact acagaaaata tgcagctatc tttctggtca cattgtcggt gtttctgcat    60

gttctccatt ccgctcctga tgtgcaggat tgcccagaat gcacgctaca ggaaaaccca   120

ttcttctccc agccgggtgc cccaatactt cagtgcatgg gctgctgctt ctctagagca   180

tatcccactc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag   240

tccacttgct gtgtagctaa atcatataac agggtcacag taatgggggg tttcaaagtg   300

gagaaccaca cggcgtgcca ctgcagtact tgttattatc acaaatctta aatgttttac   360

caagtgctgt cttgatgact gctgattttc tggaatggaa aattaagttg tttagtgttt   420

atggctttgt gagataaaac tctccttttc cttaccatac cactttgaca cgcttcaagg   480

atatactgca gctttactgc cttcctcctt atcctacagt acaatcagca gtctagttct   540

tttcatttgg aatgaataca gcattaagct tgttccactg caaataaagc cttttaaatc   600

atc                                                                 603
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<210> 12
<211> 116
<212> PRT
<213> Homo sapiens

<400> 12

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Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1               5                   10                  15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
            20                  25                  30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
        35                  40                  45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
    50                  55                  60
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Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
100 105 110

Tyr His Lys Ser
115

<210> 13
<211> 390
<212> DNA
<213> Homo sapiens

<400> 13
atgaagacac tccagttttt cttccttttc tgttgctgga aagcaatctg ctgcaatagc 60

tgtgagctga ccaacatcac cattgcaata gagaaagaag aatgtcgttt ctgcataagc 120

atcaacacca cttggtgtgc tggctactgc tacaccaggg atctggtgta taaggaccca 180

gccaggccca aaatccagaa aacatgtacc ttcaaggaac tggtatatga aacagtgaga 240

gtgcccggct gtgctcacca tgcagattcc ttgtatacat acccagtggc cacccagtgt 300

cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggcccagc 360

tactgctcct ttggtgaaat gaaagaataa 390

<210> 14
<211> 129
<212> PRT
<213> Homo sapiens

<400> 14
Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
1 5 10 15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
85 90 95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys

115 120 125

Glu

<210> 15
<211> 1342
<212> DNA
<213> Homo sapiens

<400> 15
cccggagccg gaccggggcc accgcgcccg ctctgctccg acaccgcgcc ccctggacag 60

ccgccctctc ctccaggccc gtggggctgg ccctgcaccg ccgagcttcc cgggatgagg 120

gcccccggtg tggtcacccg gcgcgcccca ggtcgctgag ggaccccggc caggcgcgga 180

gatgggggtg cacgaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtcgctccc 240

tctgggcctc ccagtcctgg gcgccccacc acgcctcatc tgtgacagcc gagtcctgga 300

gaggtacctc ttggaggcca aggaggccga gaatatcacg acgggctgtg ctgaacactg 360

cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag 420

gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc 480

tgtcctgcgg ggccaggccc tgttggtcaa ctcttcccag ccgtgggagc ccctgcagct 540

gcatgtggat aaagccgtca gtggccttcg cagcctcacc actctgcttc gggctctgcg 600

agcccagaag gaagccatct cccctccaga tgcggcctca gctgctccac tccgaacaat 660

cactgctgac actttccgca aactcttccg agtctactcc aatttcctcc ggggaaagct 720

gaagctgtac acaggggagg cctgcaggac aggggacaga tgaccaggtg tgtccacctg 780

ggcatatcca ccacctccct caccaacatt gcttgtgcca caccctcccc cgccactcct 840

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gcaatgacat ctcaggggcc agaggaactg tccagagagc aactctgaga tctaaggatg 960

tcacagggcc aacttgaggg cccagagcag gaagcattca gagagcagct ttaaactcag 1020

ggacagagcc atgctgggaa gacgcctgag ctcactcggc accctgcaaa atttgatgcc 1080

aggacacgct ttggaggcga tttacctgtt ttcgcaccta ccatcaggga caggatgacc 1140

tggagaactt aggtggcaag ctgtgacttc tccaggtctc acgggcatgg gcactccctt 1200

ggtggcaaga gccccccttga caccggggtg gtgggaacca tgaagacagg atgggggctg 1260

gcctctggct ctcatggggt ccaagttttg tgtattcttc aacctcattg acaagaactg 1320

aaaccaccaa aaaaaaaaaa aa 1342

<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

<400> 16

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Arg

<210> 17
<211> 435
<212> DNA
<213> Homo sapiens

<400> 17

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cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccgg 120

cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcatc 180

tcagaaatgt ttgacctcca ggagccgacc tgcctacaga cccgcctgga gctgtacaag 240

cagggcctgc ggggcagcct caccaagctc aagggccct tgaccatgat ggccagccac 300

tacaagcagc actgccctcc aaccccggaa acttcctgtg caacccagat tatcaccttt 360

gaaagtttca aagagaacct gaaggacttt ctgcttgtca tccccttga ctgctgggag 420

ccagtccagg agtga 435

<210> 18
<211> 144
<212> PRT
<213> Homo sapiens

<400> 18
Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
130 135 140

<210> 19
<211> 501
<212> DNA
<213> Homo sapiens

<400> 19
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tgttactgcc aggacccata tgtaaaagaa gcagaaaacc ttaagaaata ttttaatgca 120

ggtcattcag atgtagcgga taatggaact cttttcttag gcattttgaa gaattggaaa 180

gaggagagtg acagaaaaat aatgcagagc caaattgtct ccttttactt caaacttttt 240

aaaaacttta aagatgacca gagcatccaa aagagtgtgg agaccatcaa ggaagacatg 300

aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360

tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg 420

gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga 480

ggtcgaagag catcccagta a 501

<210> 20
<211> 166

<212> PRT
<213> Homo sapiens

<400> 20
Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
20 25 30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145 150 155 160

Gly Arg Arg Ala Ser Gln
165

<210> 21
<211> 1352
<212> DNA
<213> Homo sapiens

<400> 21
ctgggacagt gaatcgacaa tgccgtcttc tgtctcgtgg ggcatcctcc tgctggcagg 60

cctgtgctgc ctggtccctg tctccctggc tgaggatccc cagggagatg ctgcccagaa 120

gacagataca tcccaccatg atcaggatca cccaccttc aacaagatca cccccaacct 180

ggctgagttc gccttcagcc tataccgcca gctggcacac cagtccaaca gcaccaatat 240

cttcttctcc ccagtgagca tcgctacagc ctttgcaatg ctctccctgg ggaccaaggc 300

tgacactcac gatgaaatcc tggagggcct gaatttcaac ctcacggaga ttccggaggc 360

tcagatccat gaaggcttcc aggaactcct ccgtaccctc aaccagccag acagccagct 420

ccagctgacc accggcaatg gcctgttcct cagcgagggc ctgaagctag tggataagtt 480

tttggaggat gttaaaaagt tgtaccactc agaagccttc actgtcaact tcggggacac 540

cgaagaggcc aagaaacaga tcaacgatta cgtggagaag ggtactcaag ggaaaattgt 600

ggatttggtc aaggagcttg acagagacac agtttttgct ctggtgaatt acatcttctt 660

taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt 720

ggaccaggtg accaccgtga aggtgcctat gatgaagcgt ttaggcatgt ttaacatcca 780

gcactgtaag aagctgtcca gctgggtgct gctgatgaaa tacctgggca atgccaccgc 840

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caaggccgtg cataaggctg tgctgaccat cgacgagaaa gggactgaag ctgctggggc 1140

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<210> 22
<211> 418
<212> PRT
<213> Homo sapiens

<400> 22

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Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
20 25 30

Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
35 40 45

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
50 55 60

Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
65 70 75 80

Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
85 90 95

His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
100 105 110

Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
115 120 125

Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
130 135 140

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Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
145                 150                 155                 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
                165                 170                 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
            180                 185                 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
        195                 200                 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
    210                 215                 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
225                 230                 235                 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
                245                 250                 255

Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
            260                 265                 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
        275                 280                 285

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
    290                 295                 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
305                 310                 315                 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
                325                 330                 335

Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
            340                 345                 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
        355                 360                 365

Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
    370                 375                 380

Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
385                 390                 395                 400

Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
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Gln Lys
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<210> 23
<211> 2004
<212> DNA
<213> Homo sapiens

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tcatggctgg cagcctcaca ggtttgcttc tacttcaggc agtgtcgtgg gcatcaggtg 240

cccgcccctg catccctaaa agcttcggct acagctcggt ggtgtgtgtc tgcaatgcca 300

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tacccatggc cagctgtgac ttctccatcc gcacctacac ctatgcagac acccctgatg 660

atttccagtt gcacaacttc agcctcccag aggaagatac caagctcaag ataccctga 720

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gccacttcag caagttcatt cctgagggct cccagagagt ggggctggtt gccagtcaga 1560

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<210> 24
<211> 536
<212> PRT
<213> Homo sapiens

<400> 24

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Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
            20                  25                  30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
        35                  40                  45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
    50                  55                  60

Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
65                  70                  75                  80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
                85                  90                  95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
            100                 105                 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
        115                 120                 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
    130                 135                 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
145                 150                 155                 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
                165                 170                 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
            180                 185                 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
        195                 200                 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
    210                 215                 220

Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
225                 230                 235                 240

Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
                245                 250                 255

Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
            260                 265                 270
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Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
        275                 280                 285

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
    290                 295                 300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
305                 310                 315                 320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
                325                 330                 335

Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
            340                 345                 350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
        355                 360                 365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
    370                 375                 380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
385                 390                 395                 400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
                405                 410                 415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
            420                 425                 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
        435                 440                 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
    450                 455                 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
465                 470                 475                 480

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
                485                 490                 495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
            500                 505                 510

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
        515                 520                 525

His Thr Tyr Leu Trp His Arg Gln
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<210> 25
<211> 1726
<212> DNA
<213> Homo sapiens

<400> 25
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tgcagagatg aaaaaacgca gatgatatac cagcaacatc agtcatggct gcgccctgtg 180

ctcagaagca accgggtgga atattgctgg tgcaacagtg gcagggcaca gtgccactca 240

gtgcctgtca aaagttgcag cgagccaagg tgtttcaacg ggggcacctg ccagcaggcc 300

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acagcggaga gtggcgccga gtgcaccaac tggaacagca gcgcgttggc ccagaagccc 480

tacagcgggc ggaggccaga cgccatcagg ctgggcctgg ggaaccacaa ctactgcaga 540

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<210> 26
<211> 562
<212> PRT
<213> Homo sapiens

<400> 26

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Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
            20                  25                  30

Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
        35                  40                  45

Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
    50                  55                  60

Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
65                  70                  75                  80

Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
                85                  90                  95

Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
            100                 105                 110

Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
        115                 120                 125

Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
    130                 135                 140

Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
145                 150                 155                 160

Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
                165                 170                 175

Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
            180                 185                 190

Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
        195                 200                 205

Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
    210                 215                 220

Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
225                 230                 235                 240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
                245                 250                 255

Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
            260                 265                 270

Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
        275                 280                 285

Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr
    290                 295                 300

Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala
305                 310                 315                 320

Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro
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325 330 335

Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile
340 345 350

Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu
355 360 365

Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu
370 375 380

Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp
385 390 395 400

Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser
405 410 415

Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro
420 425 430

Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly
435 440 445

Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
450 455 460

Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His
465 470 475 480

Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr
485 490 495

Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp
500 505 510

Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
515 520 525

Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
530 535 540

Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
545 550 555 560

Arg Pro

<210> 27
<211> 825
<212> DNA
<213> Homo sapiens

<400> 27
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<210> 28
<211> 156
<212> PRT
<213> Homo sapiens

<400> 28

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			20					25					30		
Thr	Gln	Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu
		35					40					45			
Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr
	50					55					60				
Phe	Lys	Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	Gln	Leu	Gln
65					70					75					80
Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	Ala
				85					90					95	
Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile
			100					105					110		
Asn	Val	Ile	Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys
		115					120					125			
Glu	Tyr	Ala	Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp
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Ile	Thr	Phe	Cys	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr				
145					150					155					

<210> 29
<211> 7931
<212> DNA
<213> Homo sapiens

<400> 29

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Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
85 90 95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
165 170 175

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Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
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Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
        195                 200                 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
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Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225                 230                 235                 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
                245                 250                 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
            260                 265                 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
        275                 280                 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
    290                 295                 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305                 310                 315                 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
                325                 330                 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
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Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
        355                 360                 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
    370                 375                 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385                 390                 395                 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
                405                 410                 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
            420                 425                 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
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Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
    450                 455                 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465                 470                 475                 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
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His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
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Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
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Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545                 550                 555                 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
                565                 570                 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
            580                 585                 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
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Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
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Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
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Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
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Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
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Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
        675                 680                 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
    690                 695                 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705                 710                 715                 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
                725                 730                 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
            740                 745                 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg
        755                 760                 765

Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp
    770                 775                 780

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys
785                 790                 795                 800

Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser
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Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
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Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
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Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
    850                 855                 860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
865                 870                 875                 880

Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
                885                 890                 895

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
            900                 905                 910

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
        915                 920                 925

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
    930                 935                 940

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
945                 950                 955                 960

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
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Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
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Lys Gly Lys Arg Ala His Gly Pro  Ala Leu Leu Thr Lys  Asp Asn Ala
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Leu Phe  Lys Val Ser Ile Ser  Leu Leu Lys Thr Asn  Lys Thr Ser
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Asn Asn  Ser Ala Thr Asn Arg  Lys Thr His Ile Asp  Gly Pro Ser
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Leu Leu  Ile Glu Asn Ser Pro  Ser Val Trp Gln Asn  Ile Leu Glu
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Ser Asp  Thr Glu Phe Lys Lys  Val Thr Pro Leu Ile  His Asp Arg
    1055                1060                1065

Met Leu  Met Asp Lys Asn Ala  Thr Ala Leu Arg Leu  Asn His Met
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Ser Asn  Lys Thr Thr Ser Ser  Lys Asn Met Glu Met  Val Gln Gln
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Lys Lys  Glu Gly Pro Ile Pro  Pro Asp Ala Gln Asn  Pro Asp Met
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Ser Phe  Phe Lys Met Leu Phe  Leu Pro Glu Ser Ala  Arg Trp Ile
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Gln Arg  Thr His Gly Lys Asn  Ser Leu Asn Ser Gly  Gln Gly Pro
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Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile
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His Thr Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu
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Leu Ser Thr Arg Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr
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Ala Pro Val Leu Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn
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Arg Thr Lys Lys His Thr Ala His Phe Ser Lys Lys Gly Glu Glu
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Leu Pro Leu Glu Glu Thr Glu Leu Glu Lys Arg Ile Ile Val Asp
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Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser
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Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr Arg Lys Lys
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Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys

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Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly
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Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp
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Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr
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1595 1600 1605

Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys
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Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys
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Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg
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Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr
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Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser
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Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr
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Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu
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His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp
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Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr
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Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu
1835 1840 1845

Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu
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Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His
1865 1870 1875

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1880 1885 1890

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1895 1900 1905

Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn
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1940 1945 1950

Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser
1955 1960 1965

Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr
1970 1975 1980

Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr
1985 1990 1995

Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly
2000 2005 2010

Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly
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caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac 240

agcacataca cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt 300

agctctgacc aggtggaaac tcaagcctgc actcgggaac agaaccgcat ctgcacctgc 360

aggcccggct ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgcgccgctg 420

cgcaagtgcc gcccgggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg 480

tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgcagg 540

ccccaccaga tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc 600

acgtccacgt cccccacccg gagtatggcc ccaggggcag tacacttacc ccagccagtg 660

tccacacgat cccaacacac gcagccaact ccagaaccca gcactgctcc aagcacctcc 720

ttcctgctcc caatgggccc cagcccccca gctgaaggga gcactggcga cttcgctctt 780

ccagttggac tgattgtggg tgtgacagcc ttgggtctac taataatagg agtggtgaac 840

tgtgtcatca tgacccaggt gaaaaagaag cccttgtgcc tgcagagaga agccaaggtg 900

cctcacttgc ctgccgataa ggcccggggt acacagggcc ccgagcagca gcacctgctg 960

atcacagcgc cgagctccag cagcagctcc ctggagagct cggccagtgc gttggacaga 1020

agggcgccca ctcggaacca gccacaggca ccaggcgtgg aggccagtgg ggccggggag 1080

gcccgggcca gcaccgggag ctcagattct tcccctggtg gccatgggac ccaggtcaat 1140

gtcacctgca tcgtgaacgt ctgtagcagc tctgaccaca gctcacagtg ctcctcccaa 1200

gccagctcca caatgggaga cacagattcc agcccctcgg agtccccgaa ggacgagcag 1260

gtccccttct ccaaggagga atgtgccttt cggtcacagc tggagacgcc agagaccctg 1320

ctggggagca ccgaagagaa gcccctgccc cttggagtgc ctgatgctgg gatgaagccc 1380

agttaaccag gccggtgtgg gctgtgtcgt agccaaggtg ggctgagccc tggcaggatg 1440

accctgcgaa ggggccctgg tccttccagg c 1471

<210> 32
<211> 461
<212> PRT
<213> Homo sapiens

<400> 32

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Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1               5                  10                  15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20                  25                  30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35                  40                  45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50                  55                  60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65                  70                  75                  80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85                  90                  95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100                 105                 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
        115                 120                 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
    130                 135                 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145                 150                 155                 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165                 170                 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180                 185                 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195                 200                 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
    210                 215                 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225                 230                 235                 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245                 250                 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
            260                 265                 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
        275                 280                 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
    290                 295                 300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
305                 310                 315                 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
```

325 330 335

Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
340 345 350

Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
355 360 365

Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
370 375 380

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
385 390 395 400

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
405 410 415

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
420 425 430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
435 440 445

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
450 455 460

<210> 33
<211> 1475
<212> DNA
<213> Homo-sapiens

<400> 33
tccacctgtc cccgcagcgc cggctcgcgc cctcctgccg cagccaccga gccgccgtct 60

agcgccccga cctcgccacc atgagagccc tgctggcgcg cctgcttctc tgcgtcctgg 120

tcgtgagcga ctccaaaggc agcaatgaac ttcatcaagt tccatcgaac tgtgactgtc 180

taaatggagg aacatgtgtg tccaacaagt acttctccaa cattcactgg tgcaactgcc 240

caaagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga 300

atggtcactt ttaccgagga aaggccagca ctgacaccat gggccggccc tgcctgccct 360

ggaactctgc cactgtcctt cagcaaacgt accatgccca cagatctgat gctcttcagc 420

tgggcctggg gaaacataat tactgcagga acccagacaa ccggaggcga ccctggtgct 480

atgtgcaggt gggcctaaag ccgcttgtcc aagagtgcat ggtgcatgac tgcgcagatg 540

gaaaaaagcc ctcctctcct ccagaagaat taaaatttca gtgtggccaa aagactctga 600

ggccccgctt taagattatt gggggagaat tcaccaccat cgagaaccag ccctggtttg 660

cggccatcta caggaggcac cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca 720

tcagcccttg ctgggtgatc agcgccacac actgcttcat tgattaccca aagaaggagg 780

actacatcgt ctacctgggt cgctcaaggc ttaactccaa cacgcaaggg gagatgaagt 840

ttgaggtgga aaacctcatc ctacacaagg actacagcgc tgacacgctt gctcaccaca 900

acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgcag ccatcccgga 960

ctatacagac catctgcctg ccctcgatgt ataacgatcc ccagtttggc acaagctgtg 1020

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tgactgttgt gaagctgatt tcccaccggg agtgtcagca gccccactac tacggctctg 1140

aagtcaccac caaaatgctg tgtgctgctg acccacagtg gaaaacagat tcctgccagg 1200

gagactcagg gggacccctc gtctgttccc tccaaggccg catgactttg actggaattg 1260

tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac 1320

acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggt 1380

ccccagggag gaaacgggca ccacccgctt tcttgctggt tgtcattttt gcagtagagt 1440

catctccatc agctgtaaga agagactggg aagat 1475

<210> 34
<211> 431
<212> PRT
<213> Homo sapiens

<400> 34

```
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1               5                  10                  15

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
            20                  25                  30

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
        35                  40                  45

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
    50                  55                  60

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65                  70                  75                  80

Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
                85                  90                  95

Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
            100                 105                 110

Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
        115                 120                 125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
    130                 135                 140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
145                 150                 155                 160

Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
                165                 170                 175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
```

180 185 190

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
195 200 205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
210 215 220

Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
225 230 235 240

Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
245 250 255

Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
260 265 270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
275 280 285

Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
290 295 300

Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
305 310 315 320

Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
325 330 335

Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
340 345 350

Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
355 360 365

Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
370 375 380

Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
385 390 395 400

Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
405 410 415

Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
420 425 430

<210> 35
<211> 107
<212> PRT
<213> Mus musculus

<400> 35
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 36
<211> 120
<212> PRT
<213> Mus musculus

<400> 36
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 37
<211> 120
<212> PRT
<213> Mus musculus

<400> 37
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 38
<211> 106
<212> PRT
<213> Mus musculus

<400> 38
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 39
<211> 1039
<212> DNA
<213> Homo sapiens

<400> 39
tcctgcacag gcagtgcctt gaagtgcttc ttcagagacc tttcttcata gactactttt 60

ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag 120

cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg 180

ggggcgctgc tggcactggc ggccctactg caggggccg tgtccctgaa gatcgcagcc 240

ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt 300

gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg 360

actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420

gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480

cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg 540

aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccggtt cacagaggtc 600

agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac 660

gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg 720

atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc 780

ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca 840

cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgccgtt 900

gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg 960

gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc 1020

cacaccagtt gaactgcag 1039

<210> 40
<211> 282
<212> PRT
<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
165 170 175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys
275 280

<210> 41
<211> 678
<212> DNA
<213> Mus musculus

<400> 41
gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60

ttctcctgca gggccagtca gttcgttggc tcaagcatcc actggtatca gcaaagaaca 120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatgtctgg gatcccttcc 180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacac tgtggagtct 240

gaagatattg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggctcg 300

gggacaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa 360

cctggaggat ccatgaaact ctcctgtgtt gcctctggat tcattttcag taaccactgg 420

atgaactggg tccgccagtc tccagagaag gggcttgagt gggttgctga aattagatca 480

aaatctatta attctgcaac acattatgcg gagtctgtga aagggaggtt caccatctca 540

agagatgatt ccaaaagtgc tgtctacctg caaatgaccg acttaagaac tgaagacact 600

ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggc 660

accactctca cagtctcc 678

<210> 42
<211> 226
<212> PRT
<213> Mus musculus

<400> 42
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu
100 105 110

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser
115 120 125

Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val
130 135 140

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser
145 150 155 160

Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg
165 170 175

Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met
180 185 190

Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn
195 200 205

Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
210 215 220

Val Ser
225

<210> 43
<211> 450
<212> DNA
<213> Homo sapiens

<400> 43
gctgcatcag aagaggccat caagcacatc actgtccttc tgccatggcc ctgtggatgc 60

gcctcctgcc cctgctggcg ctgctggccc tctggggacc tgacccagcc gcagcctttg 120

tgaaccaaca cctgtgcggc tcacacctgg tggaagctct ctacctagtg tgcggggaac 180

gaggcttctt ctacacaccc aagacccgcc gggaggcaga ggacctgcag gtggggcagg 240

tggagctggg cgggggccct ggtgcaggca gcctgcagcc cttggccctg gaggggtccc 300

tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg 360

agaactactg caactagacg cagcccgcag gcagcccccc acccgccgcc tcctgcaccg 420

agagagatgg aataaagccc ttgaaccagc 450

<210> 44
<211> 110
<212> PRT
<213> Homo sapiens

<400> 44
Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
20 25 30

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
35 40 45

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
50 55 60

Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
65 70 75 80

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
85 90 95

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
100 105 110

<210> 45
<211> 1203
<212> DNA
<213> Hepatitis B virus

<400> 45
atgggaggtt ggtcttccaa acctcgacaa ggcatgggga cgaatctttc tgttcccaat 60

cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120

ccagattggg acttcaaccc caacaaggat cactggccag aggcaatcaa ggtaggagcg 180

ggagacttcg ggccagggtt caccccacca cacggcggtc ttttggggtg gagccctcag 240

gctcagggca tattgacaac agtgccagca gcgcctcctc ctgtttccac caatcggcag 300

tcaggaagac agcctactcc catctctcca cctctaagag acagtcatcc tcaggccatg 360

cagtggaact ccacaacatt ccaccaagct ctgctagatc ccagagtgag gggcctatat 420

tttcctgctg gtggctccag ttccggaaca gtaaaccctg ttccgactac tgtctcaccc 480

atatcgtcaa tcttctcgag gactggggac cctgcaccga acatggagag cacaacatca 540

ggattcctag gacccctgct cgtgttacag gcggggtttt tcttgttgac aagaatcctc 600

acaataccac agagtctaga ctcgtggtgg acttctctca attttctagg gggagcaccc 660

acgtgtcctg gccaaaattc gcagtcccca acctccaatc actcaccaac ctcttgtcct 720

ccaatttgtc ctggttatcg ctggatgtgt ctgcggcgtt ttatcatatt cctcttcatc 780

ctgctgctat gcctcatctt cttgttggtt cttctggact accaaggtat gttgcccgtt 840

tgtcctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt 900

cctgctcaag gaacctctat gtttccctct tgttgctgta caaaaccttc ggacggaaac 960

tgcacttgta ttcccatccc atcatcctgg gctttcgcaa gattcctatg ggagtgggcc 1020

tcagtccgtt tctcctggct cagtttacta gtgccatttg ttcagtggtt cgcagggctt 1080

tcccccactg tttggctttc agttatatgg atgatgtggt attgggggcc aagtctgtac 1140

aacatcttga gtccctttt acctctatta ccaattttct tttgtctttg ggtatacatt 1200

tga 1203

<210> 46
<211> 400
<212> PRT
<213> Hepatitis B virus

<400> 46

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
165 170 175

Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
180 185 190

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
245 250 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
290 295 300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
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Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
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<211> 799
<212> DNA
<213> Homo sapiens

<400> 47
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<210> 48
<211> 217
<212> PRT
<213> Homo sapiens

<400> 48

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			20					25					30		
Ser	Arg	Pro	Phe	Asp	Asn	Ala	Met	Leu	Arg	Ala	His	Arg	Leu	His	Gln
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Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Glu	Glu	Ala	Tyr	Ile	Pro	Lys
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Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro	Gln	Thr	Ser	Leu	Cys	Phe
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Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg	Glu	Glu	Thr	Gln	Gln	Lys
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Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser	Trp
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Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val	Phe	Ala	Asn	Ser	Leu	Val
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Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp	Leu	Leu	Lys	Asp	Leu	Glu
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Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu	Glu	Asp	Gly	Ser	Pro	Arg
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Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser	Lys	Phe	Asp	Thr	Asn	Ser
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His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	Tyr	Gly	Leu	Leu	Tyr	Cys	Phe
			180					185					190		
Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	Phe	Leu	Arg	Ile	Val	Gln	Cys
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<212> DNA
<213> Homo sapiens

<400> 49

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<212> PRT
<213> Homo sapiens

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Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu
35 40 45

Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
50 55 60

Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
65 70 75 80

Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
85 90 95

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
100 105 110

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Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
        115                 120                 125

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
    130                 135                 140

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
145                 150                 155                 160

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
                165                 170                 175

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
            180                 185                 190

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
        195                 200                 205

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
    210                 215                 220

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
225                 230                 235                 240

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
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Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
            260                 265                 270

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
        275                 280                 285

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
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Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<212>  PRT
<213>  Homo sapiens

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Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
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Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
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<210> 52
<211> 107
<212> PRT
<213> Mus musculus

<400> 52
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Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 53
<211> 119
<212> PRT
<213> Homo sapiens

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
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Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
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<212> PRT
<213> Mus musculus

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Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
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<211> 214
<212> PRT
<213> Homo sapiens

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Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 56
<211> 448
<212> PRT
<213> Homo sapiens

<400> 56
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro

195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
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Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
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<210> 57
<211> 8540
<212> DNA
<213> Homo sapiens

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cagctcagca gcctgacatc tgaggactct gcggtctatt actgtgcaag atcgacttac 360

tacggcggtg actggtactt caatgtctgg ggcgcaggga ccacggtcac cgtctctgca 420

<210> 62
<211> 140
<212> PRT
<213> Mus musculus

<400> 62
Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
50 55 60

Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
115 120 125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
130 135 140

<210> 63
<211> 1395
<212> DNA
<213> Homo sapiens

<400> 63
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acagccaagc cgcgggacat tcccatgaat cccatgtgca tttaccgctc cccggagaag 180

aaggcaactg aggatgaggg ctcagaacag aagatcccgg aggccaccaa ccggcgtgtc 240

tgggaactgt ccaaggccaa ttcccgcttt gctaccactt tctatcagca cctggcagat 300

tccaagaatg acaatgataa cattttcctg tcacccctga gtatctccac ggcttttgct 360

atgaccaagc tgggtgcctg taatgacacc ctccagcaac tgatggaggt atttaagttt 420

gacaccatat ctgagaaaac atctgatcag atccacttct tctttgccaa actgaactgc 480

cgactctatc gaaaagccaa caaatcctcc aagttagtat cagccaatcg ccttttgga 540

gacaaatccc ttaccttcaa tgagacctac caggacatca gtgagttggt atatggagcc 600

aagctccagc ccctggactt caaggaaaat gcagagcaat ccagagcggc catcaacaaa 660

tgggtgtcca ataagaccga aggccgaatc accgatgtca ttccctcgga agccatcaat 720

gagctcactg ttctggtgct ggttaacacc atttacttca agggcctgtg gaagtcaaag 780

ttcagccctg agaacacaag gaaggaactg ttctacaagg ctgatggaga gtcgtgttca 840

gcatctatga tgtaccagga aggcaagttc cgttatcggc gcgtggctga aggcacccag 900

gtgcttgagt tgcccttcaa aggtgatgac atcaccatgg tcctcatctt gcccaagcct 960

gagaagagcc tggccaaggt ggagaaggaa ctcaccccag aggtgctgca ggagtggctg 1020

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ttcagtttga aggagcagct gcaagacatg ggccttgtcg atctgttcag ccctgaaaag 1140

tccaaactcc caggtattgt tgcagaaggc cgagatgacc tctatgtctc agatgcattc 1200

cataaggcat ttcttgaggt aaatgaagaa ggcagtgaag cagctgcaag taccgctgtt 1260

gtgattgctg gccgttcgct aaaccccaac agggtgactt tcaaggccaa caggcctttc 1320

ctggttttta taagagaagt tcctctgaac actattatct tcatgggcag agtagccaac 1380

ccttgtgtta agtaa 1395

<210> 64
<211> 464
<212> PRT
<213> Homo sapiens

<400> 64

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val
1 5 10 15

Tyr Leu Leu Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys
20 25 30

His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
35 40 45

Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
50 55 60

Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
65 70 75 80

Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
85 90 95

His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
100 105 110

Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
115 120 125

Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
130 135 140

Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
145 150 155 160

Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
165 170 175

Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
180 185 190

Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys

195 200 205

Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
210 215 220

Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
225 230 235 240

Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
245 250 255

Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
260 265 270

Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
275 280 285

Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
290 295 300

Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
305 310 315 320

Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
325 330 335

Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
340 345 350

Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
355 360 365

Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
370 375 380

Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
385 390 395 400

His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
405 410 415

Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val
420 425 430

Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
435 440 445

Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
450 455 460

<210> 65
<211> 1962
<212> DNA
<213> Homo sapiens

<400> 65
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cccccggtgg ccccggccga ggccccgcac ctggtgcagg tggacgcggc ccgcgcgctg 12

tggcccctgc ggcgcttctg gaggagcaca ggcttctgcc ccccgctgcc acacagccag 18

gctgaccagt acgtcctcag ctgggaccag cagctcaacc tcgcctatgt gggcgccgtc 240

cctcaccgcg gcatcaagca ggtccggacc cactggctgc tggagcttgt caccaccagg 300

gggtccactg gacggggcct gagctacaac ttcacccacc tggacgggta cttggacctt 360

ctcagggaga accagctcct cccagggttt gagctgatgg gcagcgcctc gggccacttc 420

actgactttg aggacaagca gcaggtgttt gagtggaagg acttggtctc cagcctggcc 480

aggagataca tcggtaggta cggactggcg catgtttcca agtggaactt cgagacgtgg 540

aatgagccag accaccacga ctttgacaac gtctccatga ccatgcaagg cttcctgaac 600

tactacgatg cctgctcgga gggtctgcgc gccgccagcc ccgccctgcg gctgggaggc 660

cccggcgact ccttccacac cccaccgcga tccccgctga gctggggcct cctgcgccac 720

tgccacgacg gtaccaactt cttcactggg gaggcgggcg tgcggctgga ctacatctcc 780

ctccacagga agggtgcgcg cagctccatc tccatcctgg agcaggagaa ggtcgtcgcg 840

cagcagatcc ggcagctctt ccccaagttc gcggacaccc ccatttacaa cgacgaggcg 900

gacccgctgg tgggctggtc cctgccacag ccgtggaggg cggacgtgac ctacgcggcc 960

atggtggtga aggtcatcgc gcagcatcag aacctgctac tggccaacac cacctccgcc 1020

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gcgcagcgca cgctcaccgc gcgcttccag gtcaacaaca cccgcccgcc gcacgtgcag 1140

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ctggccagcg cccaccgccc ccagggcccg gccgacgcct ggcgcgccgc ggtgctgatc 1320

tacgcgagcg acgacacccg cgcccacccc aaccgcagcg tcgcggtgac cctgcggctg 1380

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accttcaacc tctttgtgtt cagcccagac acaggtgctg tctctggctc ctaccgagtt 1860

cgagccctgg actactgggc ccgaccaggc cccttctcgg accctgtgcc gtacctggag 1920

gtccctgtgc caagagggcc cccatccccg ggcaatccat ga 1962

<210> 66
<211> 653
<212> PRT
<213> Homo sapiens

<400> 66

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Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1               5                  10                  15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20                  25                  30

Gln Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35                  40                  45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50                  55                  60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65                  70                  75                  80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85                  90                  95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
            100                 105                 110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
        115                 120                 125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
    130                 135                 140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145                 150                 155                 160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
                165                 170                 175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
            180                 185                 190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
        195                 200                 205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
    210                 215                 220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225                 230                 235                 240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
                245                 250                 255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
            260                 265                 270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
        275                 280                 285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
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290 295 300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305 310 315 320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
325 330 335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
340 345 350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
355 360 365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
370 375 380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385 390 395 400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
405 410 415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
420 425 430

Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
435 440 445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
450 455 460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465 470 475 480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
485 490 495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
500 505 510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
515 520 525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
530 535 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545 550 555 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
565 570 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
580 585 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
595 600 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
610 615 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
645 650

<210> 67
<211> 1290
<212> DNA
<213> Homo sapiens

<400> 67
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ctcgtttcct gggacatccc tggggctaga gcactggaca atggattggc aaggacgcct 120

accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca 180

gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggt ctcagaaggc 240

tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga 300

gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat tcgccagcta 360

gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa 420

acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatgccca gacctttgct 480

gactggggag tagatctgct aaaatttgat ggttgttact gtgacagttt ggaaaatttg 540

gcagatggtt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac 600

tcctgtgagt ggcctcttta tatgtggccc tttcaaaagc ccaattatac agaaatccga 660

cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720

agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg 780

ggttggaatg acccagatat gttagtgatt ggcaactttg gcctcagctg gaatcagcaa 840

gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900

cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960

caggacccct tgggcaagca agggtaccag cttagacagg gagacaactt tgaagtgtgg 1020

gaacgacctc tctcaggctt agcctgggct gtagctatga taaaccggca ggagattggt 1080

ggacctcgct cttataccat cgcagttgct tccctgggta aaggagtggc ctgtaatcct 1140

gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact 1200

tcaaggttaa gaagtcacat aaatcccaca ggcactgttt tgcttcagct agaaaataca 1260

atgcagatgt cattaaaaga cttactttaa 1290

<210> 68
<211> 429
<212> PRT
<213> Homo sapiens

<400> 68

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Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
1               5                  10                  15

Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
            20                  25                  30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
        35                  40                  45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
    50                  55                  60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65                  70                  75                  80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
                85                  90                  95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
            100                 105                 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
        115                 120                 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
    130                 135                 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
145                 150                 155                 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
                165                 170                 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
            180                 185                 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
        195                 200                 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
    210                 215                 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
225                 230                 235                 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
                245                 250                 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
            260                 265                 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
        275                 280                 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
    290                 295                 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
305                 310                 315                 320
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Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
405 410 415

Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu
420 425

<210> 69
<211> 351
<212> DNA
<213> Homo sapiens

<400> 69
atggattact acagaaaata tgcagctatc tttctggtca cattgtcggt gtttctgcat 60

gttctccatt ccgctcctga tgtgcaggat tgcccagaat gcacgctaca ggaaaaccca 120

ttcttctccc agccgggtgc cccaatactt cagtgcatgg gctgctgctt ctctagagca 180

tatcccactc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag 240

tccacttgct gtgtagctaa atcatataac agggtcacag taatgggggg tttcaaagtg 300

gagaaccaca cggcgtgcca ctgcagtact tgttattatc acaaatctta a 351

<210> 70
<211> 116
<212> PRT
<213> Homo sapiens

<400> 70
Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1 5 10 15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
100 105 110

Tyr His Lys Ser
115

<210> 71
<211> 498
<212> DNA
<213> Homo sapiens

<400> 71
atggagatgt tccaggggct gctgctgttg ctgctgctga gcatgggcgg gacatgggca 60

tccaaggagc cgcttcggcc acggtgccgc cccatcaatg ccaccctggc tgtggagaag 120

gagggctgcc ccgtgtgcat caccgtcaac accaccatct gtgccggcta ctgccccacc 180

atgacccgcg tgctgcaggg ggtcctgccg gccctgcctc aggtggtgtg caactaccgc 240

gatgtgcgct tcgagtccat ccggctccct ggctgcccgc gcggcgtgaa ccccgtggtc 300

tcctacgccg tggctctcag ctgtcaatgt gcactctgcc gccgcagcac cactgactgc 360

gggggtccca aggaccaccc cttgacctgt gatgaccccc gcttccagga ctcctcttcc 420

tcaaaggccc ctcccccag ccttccaagc ccatcccgac tcccgggcc ctcggacacc 480

ccgatcctcc cacaataa 498

<210> 72
<211> 165
<212> PRT
<213> Homo sapiens

<400> 72
Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Leu Ser Met Gly
1 5 10 15

Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile
20 25 30

Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
35 40 45

Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val
50 55 60

Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
65 70 75 80

Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
85 90 95

Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
100 105 110

Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu

115 120 125

Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro
130 135 140

Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
145 150 155 160

Pro Ile Leu Pro Gln
165

<210> 73
<211> 165
<212> PRT
<213> Homo sapiens

<400> 73
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
20 25 30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145 150 155 160

Cys Arg Thr Gly Asp
165

<210> 74
<211> 588
<212> DNA
<213> Homo sapiens

<400> 74
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ctgcaccaaa tgaggagaat ctccccttтc ttgtgtctca aggacagaag agacttcagg 180

ttccccccagg agatggtaaa agggagccag ttgcagaagg cccatgtcat gtctgtcctc 240

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aacatgaccc tcctagacca actccacact ggacttcatc agcaactgca acacctggag 360

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gactgtgcct gggaagttgt cagaatggaa atcatgaaat ccttgttctt atcaacaaac 540

atgcaagaaa gactgagaag taaagataga gacctgggct catcttga 588

<210> 75
<211> 195
<212> PRT
<213> Homo sapiens

<400> 75

Met	Ala	Leu	Leu	Phe	Pro	Leu	Leu	Ala	Ala	Leu	Val	Met	Thr	Ser	Tyr
1				5					10						15
Ser	Pro	Val	Gly	Ser	Leu	Gly	Cys	Asp	Leu	Pro	Gln	Asn	His	Gly	Leu
			20					25					30		
Leu	Ser	Arg	Asn	Thr	Leu	Val	Leu	Leu	His	Gln	Met	Arg	Arg	Ile	Ser
		35					40					45			
Pro	Phe	Leu	Cys	Leu	Lys	Asp	Arg	Arg	Asp	Phe	Arg	Phe	Pro	Gln	Glu
	50					55					60				
Met	Val	Lys	Gly	Ser	Gln	Leu	Gln	Lys	Ala	His	Val	Met	Ser	Val	Leu
65					70					75					80
His	Glu	Met	Leu	Gln	Gln	Ile	Phe	Ser	Leu	Phe	His	Thr	Glu	Arg	Ser
				85					90					95	
Ser	Ala	Ala	Trp	Asn	Met	Thr	Leu	Leu	Asp	Gln	Leu	His	Thr	Gly	Leu
			100					105					110		
His	Gln	Gln	Leu	Gln	His	Leu	Glu	Thr	Cys	Leu	Leu	Gln	Val	Val	Gly
		115					120					125			
Glu	Gly	Glu	Ser	Ala	Gly	Ala	Ile	Ser	Ser	Pro	Ala	Leu	Thr	Leu	Arg
	130					135					140				
Arg	Tyr	Phe	Gln	Gly	Ile	Arg	Val	Tyr	Leu	Lys	Glu	Lys	Lys	Tyr	Ser
145					150					155					160
Asp	Cys	Ala	Trp	Glu	Val	Val	Arg	Met	Glu	Ile	Met	Lys	Ser	Leu	Phe
				165					170					175	
Leu	Ser	Thr	Asn	Met	Gln	Glu	Arg	Leu	Arg	Ser	Lys	Asp	Arg	Asp	Leu
			180					185					190		
Gly	Ser	Ser													
		195													